

OPTIMA 2026

XVIII. OPTIMA MEETING

The Organization for the Phyto-Taxonomic Investigation of the Mediterranean Area

22 - 26 September 2026
Nevşehir, Cappadocia, TÜRKİYE

ABSTRACT BOOK

EDITORS

Prof. Dr. K. Hüsnü Can BAŞER
Prof. Dr. Ferhat CELEP
Prof. Dr. Müberra KOŞAR



TÜBİTAK

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FOREWORD & WELCOME MESSAGE FROM THE EDITORS

Dear Colleagues and Distinguished Participants,

It is our distinct honor and privilege to welcome you to the official Abstract Book of the 18th OPTIMA Meeting, held in the historic and extraordinary setting of Nevşehir-Cappadocia, Türkiye, from September 22 to 26, 2026.

Since its inauguration in Greece in 1975, the Organization for the Phyto-Taxonomic Investigation of the Mediterranean Area (OPTIMA) has served as an essential international forum for botanists, taxonomists, pharmacognosists, and natural product scientists dedicated to Mediterranean flora. Türkiye has previously had the privilege of hosting this prestigious gathering in Istanbul (1986) and Antalya (2010). Today, we are proud to host the 18th edition in Cappadocia, a region renowned not only for its unique cultural heritage but also for its rich biodiversity.

This year's scientific program reflects the multidisciplinary essence of OPTIMA, bridging traditional botanical taxonomy with cutting-edge pharmacological, chemical, ethnobotanical, and industrial research on medicinal and aromatic plants.

This Abstract Book brings together a remarkable body of scientific work contributed by researchers representing 24 countries across the globe. The volume encompasses:

1 Plenary Lecture, setting the strategic vision for Mediterranean botanical research;

1 Tailored Speech, highlighting milestone achievements in the field;

85 Contributed Keynote and Oral Presentations, showcasing breakthrough findings across diverse disciplines; and

86 Poster Presentations, offering vibrant insights into ongoing research initiatives and innovations.

We extend our deepest gratitude to the members of the International Scientific Committee, the session chairs, and all contributing authors whose dedication and rigorous research made this comprehensive volume possible. We also convey our special thanks to our sponsors, institutional partners, and supporting staff for their unwavering commitment to the success of this congress.

We trust that the abstracts compiled in this book will serve as a valuable reference, inspiring new scientific queries, interdisciplinary collaborations, and lasting international partnerships.

We wish you all a highly engaging, productive, and memorable meeting in Cappadocia.

Sincerely,

Prof. Dr. K. Hüsnü Can Başer
Prof. Dr. Ferhat Celep
Prof. Dr. Müberra Koşar
Editors of the Abstract Book of 18th OPTIMA Meeting (2026)

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Burak Seçer (Biodiversity and Nature Conservation Association)

Congress Chairs:
Prof. Dr. K. Hüsnü Can Başer and Prof. Dr. Ferhat Celep

Congress Organization Chair:
Prof. Dr. Müberra Koşar

PREVIOUS OPTIMA MEETINGS

The XVII OPTIMA Meeting took place in Erice (Italy) the 20th-23th September 2023.

The XVI OPTIMA Meeting took place in Athens (Greece) the 2th-5th October 2019.

The XV OPTIMA Meeting took place in Motpellier (France) the 6th-11th june 2016.

The XIV OPTIMA Meeting took place in Palermo (Italy) the 9th-15th September 2013.

The XIII OPTIMA Meeting took place in Antalya (Türkiye) the 22th-27th March 2010.

The XII OPTIMA Meeting took place in Pisa (Italia) the 10th-16th September 2007.

The XI OPTIMA Meeting took place in Belgrade (Serbia and Montenegro Republic) the 5th-11th September 2004.

The X OPTIMA Meeting took place in Palermo (Italy) the 13th-19th September 2001.

The IX OPTIMA Meeting took place in Paris (France) the 11th-17th May 1998.

The VIII OPTIMA Meeting took place in Sevilla (Spain) the 25th September-1th October 1995.

The VII OPTIMA Meeting took place in Borovec (Bulgaria) the 18th-30th July 1993.

The VI OPTIMA Meeting took place in Delfi (Greece) the 10th-16th September 1989.

The V OPTIMA Meeting took place in Istanbul (Türkiye) the 8th-15th September 1986.

The IV OPTIMA Meeting took place in Palermo (Italy) the 6th-12th June 1983.

The III OPTIMA Meeting took place in Madrid (Spain) the 8th-14th September 1980.

The II OPTIMA Meeting took place in Firenze (Italy) the 23th-29th May 1977.

The I OPTIMA Meeting took place in Iraklion (Greece) the 22th-28th September 1975.

About Meeting

XVIII OPTIMA MEETING

The Organization for the Phyto-Taxonomic Investigation of the Mediterranean Area (OPTIMA) is an international association of botanists interested in the Mediterranean area. OPTIMA encompasses botany in its widest sense and deals with all groups of plants and all disciplines which have an impact on systematic studies.

The Congress consisted of three days, with Scientific sessions that focus on the main Botanical themes and include one plenary conference, two round tables, poster session on topics of significant Botanical-social impact and major issues of public interest.

Congress Venue: Nevşehir Hacı Bektaş Veli University Vali Şinasi Kuş Culture and Congress Center, Nevşehir Türkiye

Congress Schedule: 22-25 September 2026

Field Trip: 26 September 2026 Excursion

INSTITUTIONAL PARTNERS

Eastern Mediterranean University

Near East University

Kırıkkale University

Nevşehir Hacı Bektaş Veli University

Erciyes University

SCIENTIFIC PROGRAM: XVIII OPTIMA MEETING (2026)

Programme		
22-26 September 2026		
Online – Before the congress	**Meetings of the Scientific Commissions of OPTIMA**	
Tuesday, 22 September 2026		
9:00	**Welcoming of the participants and registration**	
9:00	**Joint Meeting of the Executive Council & International Board of OPTIMA (restricted)**	
10:30-11:00	**Opening Ceremony** ***President of the 18. OPTIMA Meeting:*** *Prof. Dr. Hüsnü Can Başer* ***President of the OPTIMA:*** *Prof. Dr. Francesco Maria Raimondo* ***Rector of Nevşehir Hacı Bektaş Veli University:*** *Prof. Dr. Semih Aktekin*	
11:00-12:00	***Plenary lecture*** Gonzalo Nieto Feliner - Plant systematics and evolution in the Mediterranean: Past lessons, future challenges	
12:00-12:30	***Tailored speech*** Adil Güner - Resimli Türkiye florası (The illustrated Flora of Türkiye)	
12:30-14:00	**Lunch**	
	Hall 1	**Hall 2**
14:00	**Symposium 1-** Integrating omics and bioengineering approaches in plant science ***Chairs: Erdal Bedir***	**Symposium 2-** Sustainable usage and conservation of Mediterranean plants ***Chairs: Fatih Demirci, Tiziana Ulian***
14:00–14:30	Maria Halabalaki- Metabolomic approaches in food bioactives	Joan Valles - Wild food plants and fungi in the Catalan linguistic area (and beyond): Achievements and perspectives
14:30–15:00	Anne Frary - Opium poppy multi-omics: Toward precision breeding of Benzylisoquinoline alkaloid content	Fatih Demirci - Synergy of aromatic plants and their constituents
15:00–15:30	Emre Aksoy - Integrative phenomics and genome-wide association mapping reveal iron-deficiency tolerance strategies in common bean	Paula Ros - A transboundary biodiversity information system for the conservation and sustainable use of native alpine plants in the Latin Alps
15:30–16:00		Tiziana Ulian - From global food plant diversity to Mediterranean food systems
16:00–16:15	**Coffee Break**	**Coffee Break**
16:15–16:45	Mehmet Cengiz Baloglu - Biotechnology, genome editing and omics in modern plant	Irine Danelia - The Mediterranean plant collection of the National Botanical Garden

	breeding: Advances and perspectives in Türkiye	of Georgia: Diversity, biogeographical relationships and conservation value
16:45–17:15	Emirhan Gül - Early gravitropic responses of *Hordeum vulgare* cv. "Özdemir" and *Zea mays* "Vega F1" seedlings under simulated microgravity conditions	Özgür Eminağaoğlu - An integrated model for the in situ and ex situ conservation of medicinal and aromatic plants in the Caucasus biodiversity hotspot: The Ali Nihat Gökyiğit Botanical Garden
17:15–17:30		Merve Etöz - The importance and feasibility of water harvesting in countering the adverse effects of climate change on olive production in the Mediterranean region
19:00	**Welcome cocktail**	
Wednesday, September 23, 2026		
	Hall 1	**Hall 2**
9:00	**Symposium 3**- Recent floristic studies in Mediterranean countries ***Chairs: Neriman Özhatay, Gianniantonio Domina***	**Symposium 4**- Chemical diversity of medicinal and aromatic plants and their health benefits ***Chairs: İhsan Çalış, Müberra Koşar***
09:00–09:30	Gianniantonio Domina - Assessing floristic knowledge advancement in Italy from 1978 to 2025	Funda Nuray Yalçın - Secondary metabolites targeting urological cancers
09:30–10:00	Florian Mombrial - Floristic data integration and chorological updates in North Africa: Insights from eFloraMaghreb	F. Sezer Senol Deniz - Evaluation of the effects of some plants from the Lamiaceae family grown in Türkiye against Alzheimer's Disease by *in vitro* and *in vivo* methods
10:00–10:30	Giacomo Calvia - The vascular flora of the La Maddalena Archipelago (Sardinia): Patterns of change through	Burçin Karakuzu - Phytochemical studies on the leaves of *Astragalus tmoleus* Var. *bounacanthus* and investigation of their effects on cellular senescence
10:30–11:00	Antoni Buira - Exploring the Iberian flora: patterns of species discovery, diversity and endemism	Ilgaz Akata - From Poison to Potential: A review of the toxic mushrooms of Türkiye
11:00–11:15	**Coffee Break**	**Coffee Break**
11:15–11:45	Marco D'Antraccoli - Applying next generation floristics to a Mediterranean protected area: The case of the Migliarino–San Rossore–Massaciuccoli Regional Park (Tuscany, central Italy)	Golshan Zare - Metabolomic profiling-based chemotaxonomic evaluation of the genus *Iberis* L. (Brassicaceae) in Türkiye
11:45–12:15	Abdelmonaim Homrani Bakali - Floristic research in Morocco: Recent discoveries, updated statistics and future directions	İhsan Çalış - Exploring the chemical diversity of Mediterranean plants: New natural products and recent findings from our research

12:15–12:45	Bahar Gürdal - Floristic studies in the Mediterranean basin of Türkiye	Tuğba Subaş - Investigation of the skin-related enzyme inhibitory, antioxidant activity and phenolic profile of *Satureja spicigera*
9:00-12:00	*Meeting of the enlarged OPTIMA Commission for alien plants in the Mediterranean area* ***Organizer:*** *OPTIMA Commission for Alien Plants in the Mediterranean Area* ***Chairs: Jordi López-Pujol, Carlos Gómez-Bellver, Milica Rat***	
12:45-14:00	**Lunch**	
14:00	**Symposium 5-** Integrative taxonomy ***Chairs: Musa Doğan, Božo Frajman***	**Symposium 6-** Alien plants and their impact in the Mediterranean area ***Chairs: Jordi López-Pujol, Olja Vasic***
14:00–14:30	Martina Temunovic - Combining genomic data with ecological niches informs taxonomy within *Dianthus ciliatus* and *D. sylvestris*	Carlos Gómez-Bellver - Botanical gardens as permeable systems for alien plants: Introduction, escape, and intra-garden dispersal dynamics—a case study of the Barcelona Botanical Garden.
14:30–15:00	Cyllène Chatellier - Biogeography as a formal condition for species delimitation: A case study in Mediterranean *Romulea* (Iridaceae)	Lina Podda - Conservation and restoration of Sardinian coastal habitats invaded by alien plant species
15:00–15:30	Lorenzo Peruzzi - TOI (Turrill's Omega Index) a new heuristic index for quantifying the support of a taxonomic hypothesis	Salvatore Cambria - Malta and Sicily an incomparable dimension but a surprising similar alien plant diversity
15:30–16:00	Božo Frajman - Integrative approach in resolving taxonomy and diversification of the Mediterranean *Euphorbia* (Euphorbiaceae)	Milica Rat - Towards a prioritisation framework for invasive alien plants in Serbia: From updated checklists to management planning
16:00–16:15	**Coffee Break**	**Coffee Break**
16:15–16:45	Marek Slovak - The legacy of historical hybridisation and introgression in Mediterranean endemic speciation: insights from the genera *Daphne* (Thymelaeaceae) and *Picris* (Compositae)	Ouafae Benkhnigue - Floristic and ecological study of alien flora of Morocco
16:45–17:15	Maria-Anna Vasile - Integrative taxonomy of Boraginales across scales: Resolving relationships from global family-level patterns to species-level diversification in Mediterranean radiations	Javier Martínez-Fuentes - New steps on the cataloging of alien flora in the Pyrenees
17:15–17:45	Emine Akalın - Integrative taxonomy and recent systematic revisions of species-rich Apiaceae genera in Türkiye	Salma Shaltout - Reassessment of the worst invasive alien plant species according to IUCN EICAT criteria in Egypt
17:45–18.15		Mine Koçyiğit - Melissopalynological insights into honey bee foraging on invasive alien plants in Türkiye
18:15–19:30	**Poster Session (Organized by Benito Valdés)**	
	Thursday, September 24, 2026	

	Hall 1	Hall 2
9:00	**Symposium 7-** New natural sources for medicinal usage: Marine organisms, fungi, endophytes, etc. ***Chairs: İlkay Erdoğan Orhan, Funda Nuray Yalçın***	**Symposium 8-** Biosystematics in the Mediterranean area (Young Scientist Symposium) ***Chairs: Karol Marhold, Christoph Oberprieler, Lorenzo Peruzzi***
09:00–09:30	Vassilios Roussis- The red alga *Laurencia*: Where biodiversity meets chemodiversity	Jacopo Franzoni - Advances in the systematics of wild carnations (*Dianthus*) in the central Mediterranean
09:30–10:00	Leandros Skoultsounis - Indigoids: From natural dyeing agents to selective kinase inhibitors	Murat Erdem Güzel - On the identity of *Crepis dioscoridis* (Asteraceae): Evidence from Greece and Türkiye
10:00–10:30	Ilkay Erdogan Orhan - Promising potential of natural products from Turkish marine and fresh water ecosystem	Osman Erol - Rapid speciation and centers of diversity: Case studies across the genus *Crocus* (Iridaceae) in Türkiye
10:30–11:00	Erdal Bedir - Fungal biotransformation: A route to novel and bioactive metabolites	Jose Luis Villar - Current status of *Tamarix* taxonomy in the Mediterranean region: Critical groups and future scopes
11:00–11:15	**Coffee Break**	**Coffee Break**
11:15–11:45	Anna Beresova Guttova - Climate and substrate filtering in Mediterranean lichens: a case study from the genus *Solenopsora*	Pia Donhauser - Integrative species delimitation in the North-West African genus *Rhodanthemum* (Compositae, Anthemideae)
11:45–12:15	Efstathia Ioannou - New bioactive diterpenes from brown algae of the genus *Dictyota* from the Aegean and Ionian seas	Batıkan Günal - An Assessment of the taxonomic complexity of the *Erigeron acris* group in Türkiye
12:15–12:45	Mustafa Ünver Kurt - Marine-derived *Streptomyces* sp. L8A39 from the İzmir peninsula as a source of cytotoxic metabolites against drug-Resistant A549 cell line	Tuğkan Özdöl - Revisiting *Campanula* L. (Campanulaceae) in Türkiye: Integrative taxonomy and insights into diversity, endemism, and phylogenetic complexity
12:45–13:00	Zehra Torun - Hidden jewel in the Mediterranean: Anticancer potential of marine-associated fungus *Fusarium oxysporum* extract	Seher Güven - Palynological characteristics of the registered tea (*Camellia sinensis*) cultivars in Türkiye
13:00-14:00	**Lunch**	
14:00	**Symposium 9-** Beyond preservation: The evolving functions of Mediterranean herbaria ***Chair: Adil Güner***	**Symposium 10-** Recent advances in Lamiaceae science ***Chairs: Tuncay Dirmenci, Chunlei Xiang, Bryan Drew***
14:00–14:30	Erich Helmut Freitag - The genus *Ephedra* (Ephedraceae, Gnetales) in Tunisia	Chunlei Xiang - Taxonomy, phylogenomics, biogeography and evolution of *Phlomoides* (Lamiaceae, Lamioideae)

14:30–15:00	Igor Boršić - The herbarium collection of the Croatian Natural History Museum – CNHM as a source of data on the vascular flora of Mediterranean Croatia	Selami Selvi - From past to present: Ethnobotanical uses of Lamiaceae species in the Mediterranean region
15:00–15:30	Alessio Papini - The massive data production by scanning of the main Italian herbaria	Hye-Kyoung Moon - Repeated gynodioecy: A window into reproductive evolution in Lamiaceae
15:30–16:00	Salvatore Tomasello - Museomics and type material disentangle long-debated species delimitation in the taxonomically complex *Xanthium* subsect. *Campylorrhyncha*	Fei Zhao - Plastome and Multi-Locus Phylogeny of *Ajuga* (Lamiaceae): Reassessing Infrageneric Classification
16:00–16:15	**Coffee Break**	**Coffee Break**
16:15–16:45	Euro-Med Editorial Committee Meeting (with 10 participants)	Bryan Drew - History of Lamiaceae in the Mediterranean region
16:45–17:15		Miguel Campos - Incomplete lineage sorting and pulsed introgression drive extensive cytonuclear discordance in the rapidly radiating *Sideritis* sect. *Empedoclia* (Lamiaceae)
17:15-17.45	Euro-Med Round Table Meeting (with 20 participants)	Taner Özcan - *Anatolia*: Resolving a long-standing taxonomic puzzle in Menthinae
17:45-18:15		
20:00	**Gala Dinner**	
	Friday, September 25, 2026	
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9:00	**Symposium 11-** Mediterranean forests: Ecology & challenges ***Chairs: Ünal Akkemik, Stephan Woodward***	**Symposium 12-** Molecular studies may provide help to taxonomy ***Chairs: Barış Özüdoğru, Christoph Oberprieler***
09:00–09:30	Stephan Woodward - Mediterranean forests under pressure: Climate change, biological invasions, and emerging risks to forest ecosystems	Karol Marhold - Multiple hybrid zones involving four *Cardamine* species and their triploid progeny: Another nascent neopolyploids in action?
09:30–10:00	Candan Aykurt - Phylogenetic diversity patterns in Mediterranean mountain plant communities: A case study from the Western Taurus Mountains (Türkiye)	Dörte Harpke - A phylogenomic framework for understanding diversification, genome evolution, and karyotype changes in *Crocus*
10:00–10:30	Çağatay Tavsanoğlu - Mediterranean forests under changing fire regimes: regeneration, resilience and emerging challenges	Ozan Şentürk - Phylogenomic reassessment of the tribe Genisteae (Leguminosae): New insights into an iconic Mediterranean plant group
10:30–11:00	Funda Özdemir Değirmenci - Genetics and conservation of native *Populus* and *Salix* Species in Turkish riparian forests:	Maria Ángeles Alonso-Vargas - Molecular phylogeny of the genus *Frankenia*

	Insights from Nuclear SSRs and plastid barcodes	(Frankeniaceae): New evidence from Eurasia and Africa
11:00–11:15	**Coffee Break**	**Coffee Break**
11:15–11:45	Ünal Akkemik - The effect of climate change on some forest trees and their growth in the Mediterranean basin of Türkiye	Tim Böhnert - From topology to taxonomy: Phylogenomics and genus delimitation in Mediterranean hyacinths
11:45–12:15	Deniz Aygören Uluer - A Preliminary molecular phylogeny of the genus *Thalictrum*: Insights into Turkish taxa	Ruifang An - Phylogenomics and cytogenetics reveal differentiated lineages in the *Crocus serotinus* complex
12:15–12:45		Jordi Lopez-Pujol - Molecular studies in support of taxonomy: examples from the Western Mediterranean Basin
12:45-13:00		Emrullah Yılmaz - Genome wide RADseq data provide new insights into species boundaries in the Noccaea densiflora complex
12:45-14:00	**Lunch**	
14:00	Closing Ceremony and General Meeting of OPTIMA	
15:00	Sightseeing to Cappadocia cites	
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9:00	Excursion (Organized by Hayri Duman and Ferhat Celep)	

XVIII OPTIMA MEETING (2026)- ORAL PRESENTATIONS

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5.6	Integrative taxonomy of Boraginales across scales: Resolving relationships from global family-level patterns to species-level diversification in Mediterranean radiations	Maria-Anna Vasile	67-68
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Plenary Lecture

Plant systematics and evolution in the Mediterranean: Past lessons, future challenges

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The last four decades, bridging the 20th and 21st centuries, have been an eventful period for almost any scientific discipline. In this talk, I will reflect on the changes in goals, methods, and achievements that I have witnessed in the field of plant systematics and evolution in the Mediterranean over the last forty years, drawing on my own experience. I will argue that the fundamental questions remain. Specifically: what are the recognizable biological entities within our groups of interest? What are their morphological, reproductive, molecular, chemical and ecological attributes and patterns of variation? How have changes over time and across space shaped their current distribution? What are the relationships between them and their congeners? What evolutionary processes underlie their current diversity? What are their chemical and medicinal properties? How can they be best conserved? There are countless and substantial improvements in all aspects. Some involve equipment, not just scientific instruments, but also everyday tools such as mobile phones and personal computers, which were unavailable in the 1980s. Other improvements involve new conceptual perspectives, such as tree thinking, phylogeography, the thorny integration of molecular evolution, genomics and morphology, and the importance of natural hybridization in shaping current diversity. The big question, then, is how these improvements — particularly in analytical methods, the amount and management of data, genome evolution and bioinformatics — have affected our understanding of plant systematics and evolution. I will argue that insights into fundamental questions have opened new avenues and encouraged the formulation of new questions in parallel with addressing challenges such as biodiversity loss.

Keywords: Evolution, history of science, Mediterranean, Plant Systematics.

Tailored Speech

Resimli Türkiye florası (The illustrated flora of Türkiye)

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General information regarding the Resimli Türkiye Florası (Illustrated Flora of Türkiye), which is currently in preparation, will be provided, along with updates on recent developments.

Keywords: Resimli Türkiye Florası, Illustrated Flora of Türkiye.

Symposium 1- Integrating omics and bioengineering approaches in plant science

Chairs: Erdal Bedir

1.1 Maria Halabalaki- Metabolomic approaches in food bioactives

1.2 Anne Frary - Opium poppy multi-omics: Toward precision breeding of Benzylisoquinoline alkaloid content

1.3 Emre Aksoy - Integrative phenomics and genome-wide association mapping reveal iron-deficiency tolerance strategies in common bean

1.4 Mehmet Cengiz Baloglu - Biotechnology, genome editing and omics in modern plant breeding: Advances and perspectives in Türkiye

1.5 Emirhan Gül - Early gravitropic responses of *Hordeum vulgare* cv. "Özdemir" and *Zea mays* cv. "Vega F1" seedlings under simulated microgravity conditions

1.1

Metabolomic approaches in food bioactives

Maria Halabalaki (0000-0001-5620-0165)

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Food matrices contain a remarkable chemical diversity of metabolites and bioactive constituents, whose comprehensive characterization and biological evaluation remain challenging. Metabolomics provides a powerful approach to address this complexity, enabling the global investigation of food composition while supporting the discovery and characterization of compounds of biological relevance.

Our research focuses on the development and application of complementary NMR-based and LC-HRMS/MS-based metabolomic approaches, and, importantly, on their integration to achieve broader metabolome coverage and higher confidence in metabolite annotation. We have applied these strategies to diverse food matrices for the discovery of bioactive constituents, including the use of HETCA as a metabolomics-guided approach for linking chemical composition with biological activity and prioritizing active compounds in complex mixtures. A central aspect of our work is also the improvement of structural confidence in metabolite identification. In this context, we have applied statistical methods such as STOCSY (Statistical Total Correlation Spectroscopy) and SHY (Statistical Heterospectroscopy) to exploit correlations within and between analytical platforms, providing complementary evidence for metabolite annotation and reducing the risk of erroneous structural assignments.

Beyond the characterization and discovery of food bioactives, we are applying integrated metabolomic approaches to investigate their bioavailability, biotransformation and metabolism**,** thereby connecting their occurrence in foods with their fate in biological systems. Overall, our work illustrates how the integration of NMR, LC-HRMS/MS, activity-guided metabolomics and correlation-based strategies can provide a comprehensive workflow from food chemical profiling and bioactive discovery to confident identification and understanding of biological fate.

Keywords: Food bioactives; NMR-based metabolomics; LC-HRMS/MS; Integrated metabolomics; HETCA

1.2

Opium poppy multi-omics: Toward precision breeding of Benzylisoquinoline alkaloid content

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Opium poppy (*Papaver somniferum*) produces pharmaceutically significant benzylisoquinoline alkaloids (BIAs) including morphine, codeine, and noscapine. While much research has been done on chemical synthesis of BIAs, the only commercially viable source is the opium poppy plant. Turkiye is a center of origin of opium poppy and, currently, is one of a handful of countries that allow legal cultivation and BIA production. The BIA yield of Turkish cultivars, however, lags behind that of other countries. Effective and efficient breeding of opium poppy requires thorough genetic, phenotypic, and metabolic characterization of existing cultivars and germplasm. To this end, we developed both expressed sequence tag simple sequence repeat (EST-SSR) markers and genomic SSR markers and used them to assess genetic diversity in Turkish opium poppy. These resources were then applied to identify loci associated with morphine content and agronomic traits including seed yield. While genomics approaches have revealed many of the genes controlling the BIA synthesis pathway, there is still much that needs to be decoded before targeted breeding approaches such as gene editing can be effectively applied. Thus, our current research focuses on integrating proteomic, metabolomic, and transcriptomic data from three Turkish cultivars with distinct BIA profiles. To date, LC-MS/MS and HPLC results have revealed differentially expressed proteins that correlate with the cultivars' unique BIA contents. The addition of transcriptomics data will then allow us to decipher the complex relationships among gene, mRNA, protein, and BIA content in opium poppy. Such knowledge will reveal key targets for further investigation, molecular breeding, and metabolic engineering.

Keywords: Opium poppy, Benzylisoquinoline, Multi-omics

1.3

Integrative phenomics and genome-wide association mapping reveal iron-deficiency tolerance strategies in common bean

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Iron (Fe) deficiency chlorosis severely constrains common bean productivity in calcareous and alkaline soils, yet the genetic architecture linking root acquisition strategies with shoot performance remains poorly resolved. We integrated multidimensional phenotyping and genome-wide association analysis to identify accessions, loci, and candidate genes underlying Fe deficiency tolerance in Turkish common bean germplasm. A panel of 133 landraces and three commercial cultivars from 19 provinces of Türkiye was grown hydroponically under Fe-sufficient and Fe-deficient conditions for 13 days. Chlorophyll concentration, SPAD index, leaf area, biomass allocation, root ferric chelate reductase (FCR) activity, and root-system architecture were quantified. Treatment-responsive phenotypes were associated with 7,900 DArT-seq markers using GAPIT, followed by candidate-gene mining within 100-kb windows and gene ontology analysis. Iron deficiency revealed extensive phenotypic diversity and contrasting adaptive strategies. Most accessions showed reduced root length and architectural traits, whereas tolerant accessions maintained more robust root systems. FCR activity increased by 16.6% but was not significantly correlated with other traits, indicating that biochemical Fe reduction and morphological root remodelling represent partly independent responses. GWAS detected seven significant markers associated with FCR activity, root fresh weight, and total root area on different chromosomes. Candidate-gene analysis highlighted regulators of root development, nutrient sensing, stress signalling, metal transport, and post-transcriptional control, including *FERONIA, ROOT MERISTEM GROWTH FACTOR 2, CHLOROPLAST MANGANESE TRANSPORTER 1, PHYTOCYSTATIN 2*, and *PUMILIO 8*. Protein-protein interaction analysis indicated potential interactions between these candidates and Fe-homeostasis proteins. RT-qPCR analysis of roots from five selected tolerant and five sensitive accessions revealed significantly greater Fe-deficiency-induced expression of the target genes in the tolerant accessions. This integrated framework distinguishes complementary tolerance mechanisms overlooked by conventional chlorosis-based screening. These findings connect physiological and architectural phenotypes with genomic variation, providing testable targets for functional validation, marker-assisted selection, and precision bioengineering of Fe-efficient common bean cultivars adapted to Fe-limiting soils.

Keywords: Iron deficiency, GWAS, *Phaseolus vulgaris*, RSA, DArT-seq markers

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1.4

Biotechnology, genome editing and omics in modern plant breeding: Advances and perspectives in Türkiye

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Modern plant breeding is increasingly shaped by biotechnology, genome editing, molecular breeding, and high-throughput omics technologies, which provide new opportunities to improve crop productivity, quality, and resilience. Conventional breeding remains fundamental; however, the complexity and polygenic nature of traits such as yield, stress tolerance, disease resistance, and developmental plasticity often require complementary molecular approaches [1]. Marker-assisted selection has become an important strategy for accelerating breeding programs by enabling the early identification of plants carrying genomic regions associated with desirable traits. Advances in next-generation sequencing have further expanded these possibilities through genome, transcriptome, proteome, metabolome, and epigenome analyses. The integration of these datasets can reveal molecular networks underlying plant growth, development, productivity, and responses to biotic and abiotic stresses. In particular, transcriptomic and epigenomic approaches provide valuable information on how environmental conditions influence gene regulation and plant adaptation. Genome editing technologies, particularly CRISPR/Cas-based systems, have introduced new possibilities for targeted modification of genes controlling agronomically important characteristics. Compared with conventional genetic modification, precise genome editing can facilitate the development of targeted genetic changes and accelerate the functional characterization of candidate genes. These approaches are increasingly relevant for improving resistance to pathogens, tolerance to drought, salinity and temperature stress, and traits associated with yield and quality [2]. Türkiye has considerable potential to integrate these technologies into contemporary breeding programs because of its diverse agroecological conditions, extensive crop diversity, and established agricultural research infrastructure. This review summarizes recent applications of biotechnology, molecular breeding, genome editing, and omics technologies in plant breeding in Türkiye and discusses their potential contributions to genetic improvement, climate resilience, sustainable crop production, and the development of next-generation breeding strategies.

Keywords: Plant breeding; Biotechnology; Genome editing; Omics technologies; Molecular breeding

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1.5

Early gravitropic responses of *Hordeum vulgare* L. cv. "Özdemir" and *Zea mays* L. cv. "Vega F1" seedlings under simulated microgravity conditions

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Gravity regulates plant architecture and organ orientation. This study investigates gravitropic responses and growth kinetics of *Zea mays* L. cv. "Vega F1" and *Hordeum vulgare* L. cv. "Özdemir" seedlings under simulated microgravity (SMG) with a 3D clinostat operated at inner and outer axis speeds of 4.0 and 1.8 rpm, respectively. Roots were standardized to 1 cm at onset; *H. vulgare* growth was tracked retrospectively from 24 h back to emergence at 12 h. Control and clinorotated groups were imaged at 4 h intervals over 24 h; lengths were measured in ImageJ. Two of four *H. vulgare* controls lacking measurable roots at t = 0–8 h were excluded; other groups retained n = 4. In Z. mays, SMG enhanced root elongation (61.15 vs. 54.76 mm) and elongation rate (2.05 vs. 1.84 mm/h), and induced shoot emergence (7.01 mm) vs. complete suppression in controls (0.00 mm). In *H. vulgare*, SMG reduced root elongation (23.98 vs. 34.15 mm, control) and elongation rate (0.62 vs. 0.93 mm/h); shoot elongation was similarly suppressed (7.44 vs. 17.89 mm).Gravitropic setpoint angles (GSA) were disrupted in both: *Z. mays* roots shifted from a 90° vertical baseline to 166° under SMG (shoot curvature up to 121°), while *H. vulgare* roots shifted from 37° (control) to 116° (shoot curvature up to 141°), consistent with an antigravitropic offset reported in clinorotated cereal (wheat, rice) roots.These findings indicate accelerated *Z. mays* growth under SMG, whereas H. vulgare shows root and shoot suppression alongside GSA disruption, suggesting species-specific rather than uniformly stimulatory responses to altered gravity vectors during early development. Preliminary data (n = 2–4 per group); statistical validation with expanded replication is ongoing.

Keywords: Simulated microgravity, Clinostat, Gravitropism, *Zea mays*, *Hordeum vulgare*

Symposium 2- Sustainable usage and conservation of mediterranean plants

Chairs: Fatih Demirci, Tiziana Ulian

2.1 Joan Valles - Wild food plants and fungi in the Catalan linguistic area (and beyond): Achievements and perspectives

2.2 Fatih Demirci - Synergy of aromatic plants and their constituents

2.3 Paula Ros - A transboundary biodiversity information system for the conservation and sustainable use of native Alpine plants in the Latin Alps

2.4 Tiziana Ulian - From global food plant diversity to Mediterranean food systems

2.5 Irine Danelia - The Mediterranean plant collection of the National Botanical Garden of Georgia: Diversity, biogeographical relationships and conservation value

2.6 Özgür Eminağaoğlu - An integrated model for the in situ and ex situ conservation of medicinal and aromatic plants in the Caucasus biodiversity hotspot: The Ali Nihat Gökyiğit Botanical Garden

2.7 Merve Etöz - The importance and feasibility of water harvesting in countering the adverse effects of climate change on olive production in the Mediterranean region

2.1

Wild food plants and fungi in the Catalan linguistic area (and beyond): Achievements and perspectives

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Food plants and fungi represent an important part of everyday human and animal diets. Among them, wild taxa play a significant role. Wild food plants are relevant to human societies, even if, in industrialised territories, their uses have dramatically decreased in the last decades. In addition, in many cases, they are ancestors or relatives of domesticated food plants, crucial in case of genetic erosion of conventional cultures, and, in some others, they are potential new crops that could increase the agronomical reach. Wild food fungi are relevant as edible and, conversely to plants, their uses are maintained, almost in mycophylous areas, even in industrialised zones.

Since the 1990s, our research team on Catalan ethnobotany studies the popular knowledge on plants and fungi in the Catalan linguistic area (CLA), including five states: Andorra (the whole country), France (the Eastern Pyrenees department), Italy (the city of l'Alguer/Alghero, in Sardinia), and Spain (Balearic Islands, Carxe area in Murcia, Catalonia, eastern strip of Aragon, Valencia). Our database comprises more than 250.000 names and uses reports from more than 4,300 informants about more than 2.000 taxa, one part of which (including food uses) is publicly accessible at https://etnobotanica.iec.cat. Reviews are available for wild food plants [1] and fungi [2] in this geographical and cultural area.

In this communication, after a state-of-art of wild food plants and fungi in the Catalan linguistic area and their perspectives, the following subjects will be addressed: 1) Plants used to elaborate beverages. 2) Plants used to feed animals. 3) The ethnobotany of a linguistic island within a geographical island, l'Alguer (Sardinia). 4) Plants and fungi in the Corpus of the Catalonian cuisine. 5) Food Lamiaceae in the Mediterranean area.

Keywords: Catalan linguistic area, Ethnobotany, Ethnomycology, Wild food fungi, Wild food plants

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[1] Gras, A. et al. *Foods*, 2021, 10, 61.
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2.2

Synergy of aromatic plant constituents

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Essential oils from aromatic plants have wide range of modern functions and applications. In this present work, binary combinations of limonene with carvacrol, thymoquinone, camphor and α-pinene were evaluated using *in vitro* antioxidant, antimicrobial and anti-inflammatory assays for their synergistical potential [1]. Initially antioxidant activities were tested at concentrations ranging from 0.078 to 10 mM using DPPH• and ABTS• radical scavenging assays. Combination interactions were analyzed using the ZIP, Bliss, Loewe, and HSA reference *in silico* models via the SynergyFinder software [2]. Also a selection of four pathogenic bacteria and *Candida albicans* were used for *in vitro* antimicrobial screening. The anti-inflammatory activities using the 5-LOX enzyme of the combinations exhibiting synergistic effects in both tests were subsequently evaluated. Overall, synergistic effects of limonene with carvacrol and thymoquinone were remarkable. This presentation will elaborate the efficacy of systematic combinations of important essential oil components.

Keywords: Monoterpenes, Checkerboard, Bioactivity, *In silico*.

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2.3

A transboundary biodiversity information system supporting the conservation and sustainable use of native plants in the Latin Alps

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The Latin Alps, extending across the western Alps of Italy and France within the ALCOTRA (Alpes Latines de Coopération Transfrontalière) cooperation area, represent a remarkable biogeographical transition zone where Alpine and Mediterranean floristic elements converge. This region harbours exceptional plant diversity, including native species of ecological and cultural value that contribute to local traditions and biocultural heritage. However, botanical, ecological and ethnobotanical information remains dispersed among heterogeneous national and regional datasets, hindering biodiversity conservation and the sustainable use of native plant resources. Within the Interreg VI-A France–Italy ALCOTRA project COrALp ("Edible and ornamental plants from the spontaneous flora of the Latin Alps: Protecting and enhancing biodiversity for a greater connection between cities and mountains"), we are developing a multidisciplinary biodiversity information system integrating taxonomic, ecological, ethnobotanical, conservation and horticultural data.

A harmonised checklist of vascular plants was generated through the taxonomic reconciliation of Italian and French botanical datasets using the World Checklist of Vascular Plants (WCVP). The database includes 5,441 plant species representing 1,157 genera and 161 families. Literature review and data integration identified 1,572 wild food plant taxa, together with information on their distribution, habitats, traditional uses, conservation status, propagation requirements and phytochemical properties.

The system also supports research on priority species for conservation and sustainable valorisation. Preliminary germination experiments on Blitum bonus-henricus (L.) Rchb., using seed collections from four populations (three Italian and one French), revealed differences in germination behaviour under contrasting temperature regimes, highlighting the importance of population provenance for developing effective propagation protocols.

By integrating biodiversity informatics, ethnobotany, seed biology and horticultural research, COrALp provides an evidence-based model supporting the conservation and sustainable use of native plant diversity across the Latin Alps, with potential application to other Mediterranean mountain regions.

Keywords: Biodiversity informatics; Latin Alps; Wild food plants; Biocultural heritage; Seed germination

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2.4

From global food plant diversity to Mediterranean food systems

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Global food systems face the dual challenge of ensuring adequate nutrition while responding to biodiversity loss, environmental change and increasing pressure on natural resources. Despite the enormous diversity of plants with food potential, human diets remain heavily dependent on a small number of major crops. The *World Checklist of Useful Plant Species* documents 7,039 plant species with recorded human food uses [1,2]. Preliminary findings from the *World Checklist of Food Plants* 2026 identify 26,622 food plant taxa [3], highlighting the largely untapped potential of plant diversity for dietary diversification and resilient food systems.

This presentation provides a global overview of the potential of Wild Food Plants (WFPs) to contribute to food security, nutrition, sustainable food systems and biodiversity conservation, before focusing on the Mediterranean region, where a recent comprehensive checklist documents 2,716 wild edible plant taxa [4].

A case study from the Eastern Mediterranean illustrates how plant conservation can be integrated with food-system sustainability through the ResMed project, using the WFP Akkoub (*Gundelia tournefortii* L.) as an example. The approach links traditional knowledge with *ex situ* conservation through seed banking and seed biology research, propagation in local nurseries, and *in situ* conservation through planting seedlings in restored traditional agricultural terraces. These activities are complemented by research on nutrients and bioactive compounds, as well as the promotion of sustainable WFP utilisation [5]. The approach provides a model adaptable to other Mediterranean WFPs.

Unlocking the potential of WFPs requires collaboration among botanists, conservation practitioners, agronomists, nutritionists, ethnobotanists, local communities and policymakers. Integrating *in situ* and *ex situ* conservation with sustainable use, cultivation, research and community engagement can strengthen biodiversity while supporting diverse, culturally appropriate and resilient food systems [2].

Keywords: Wild Food Plants; Food Plant Diversity; Mediterranean Flora; Plant Conservation; Traditional Knowledge

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2.5

The Mediterranean plant collection of the National Botanical Garden of Georgia: Diversity, biogeographical relationships and conservation value

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Georgia harbours an exceptionally rich and biogeographically complex flora shaped by its position at the convergence of the Euro-Siberian, Mediterranean, and Irano-Turanian floristic regions [1-4]. Although the country is not formally included in the Mediterranean Floristic Region, numerous Mediterranean and sub-Mediterranean elements occur naturally, particularly in western and southern Georgia, together with temperate, Euxine, and Tertiary relict taxa. These patterns reflect long-standing biogeographical links between the Caucasus and the Mediterranean Basin, including shared evolutionary history, migration through Anatolia, and persistence in major refugia [5-12].

The Mediterranean Basin is one of the world's major biodiversity hotspots, with exceptional species richness and endemism, making living collections of Mediterranean plants particularly important for ex situ conservation, research, and the preservation of drought-adapted germplasm [13-17].

The introduction of Mediterranean plants to the Tiflis Botanical Garden, the predecessor of the National Botanical Garden of Georgia (NBGG), began in the mid-nineteenth century. A dedicated Mediterranean collection was established in 1901–1902. Today, the collection occupies approximately 2.8 ha on the southern slopes of the Sololaki Range, while additional Mediterranean-affiliated taxa are represented throughout other living collections of the Garden [18-20].

The analysed collections comprise 178 woody taxa belonging to 45 families and 87 genera, and 358 herbaceous taxa belonging to 61 families and 220 genera. Among the woody taxa, 125 occur naturally in Georgia and 53 are introduced. After accounting for synonyms, approximately 50 introduced woody species are not native to the country. These taxa represent 11 chorological elements, with Mediterranean, West Mediterranean, East Mediterranean, and Balkan elements predominating.

The collection has considerable conservation value. It includes globally threatened woody taxa such as *Abies numidica* (CR), *Abies pinsapo*, *Cedrus atlantica*, *Liquidambar orientalis*, and *Abies nordmanniana* subsp. *equi-trojani* (EN), *Cedrus libani* (VU), and *Abies cilicica* (NT), as well as geographically restricted national and regional endemics.

The Mediterranean collections of NBGG therefore constitute an important *ex situ* resource for comparative biogeographical, ecological, and conservation research, while also providing valuable material for studies of plant adaptation and resilience under ongoing climate change.

Keywords: Georgia; Mediterranean flora; *ex situ* conservation; Living Plant Collections; Plant Biodiversity; Biogeography; Chorological Elements; Threatened Species; Drought-Adapted Germplasm.

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2.6

An integrated model for the in situ and ex situ conservation of medicinal and aromatic plants in the Caucasus biodiversity hotspot: The Ali Nihat Gökyiğit Botanical Garden

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Artvin Province, located within the Caucasus Biodiversity Hotspot, is one of the richest floristic regions in Türkiye, harbouring approximately 2,727 vascular plant taxa, including nearly 850 medicinal and aromatic plant (MAP) species. However, climate change, habitat loss, land-use change, and intensive harvesting from natural populations pose significant threats to this exceptional plant diversity. Therefore, effective conservation of plant genetic resources requires the integration of in situ conservation strategies with ex situ conservation practices implemented in botanical gardens. The Ali Nihat Gökyiğit Botanical Garden (ANGBB) of Artvin Çoruh University has developed an integrated model for the conservation, scientific research, and sustainable utilization of medicinal and aromatic plants. Floristic surveys, seed collection, and plant material sampling conducted in natural populations are used to identify priority species, while collected materials are incorporated into long-term conservation programmes through living collections, seed collections, and cultivation areas established within the botanical garden. Species identification is verified using DNA barcoding, and in vitro propagation techniques are applied where appropriate to support the conservation of selected taxa. These conservation activities are further strengthened by research greenhouses, demonstration gardens, and the Plant Processing and Product Development Units established under the Regional Development-Oriented Specialization Programme of Artvin Çoruh University. This infrastructure enables the production of essential oils, hydrolates, plant extracts, and other value-added products from cultivated medicinal and aromatic plants, thereby reducing harvesting pressure on natural populations while promoting sustainable production and rural development. In conclusion, the Ali Nihat Gökyiğit Botanical Garden represents an exemplary botanical garden model that integrates conservation, scientific research, cultivation, and value-added product development. This integrated approach demonstrates that biodiversity conservation and sustainable utilization can be successfully implemented together, providing a practical model for safeguarding medicinal and aromatic plant resources while supporting regional development.

Keywords: Artvin, ANGBB, ex-situ, Medicinal and Aromatic plants, Türkiye

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2.7

The importance and feasibility of water harvesting in countering the adverse effects of climate change on olive production in the Mediterranean region

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The Mediterranean Basin is becoming increasingly vulnerable in terms of crop production, water management, and sustainability due to growing climate variability. Traditional ecological methods such as water harvesting are becoming increasingly important, particularly in production areas where irrigation is not available. This is a key practice within the framework of adaptation to climate change. Water harvesting—which increases soil water-holding capacity, reduces surface water runoff, minimizes erosion, and boosts crop production by raising soil moisture levels—is a recommended practice, particularly in arid, semi-arid, and sloping areas. This study covers the evaluation of findings from 2023–2025 at a Gemlik olive (*Olea europaea* L.) plantation established in 2020. The research is based in Köyceğiz (Muğla), where the Mediterranean climate prevails but the pronounced effects of summer drought are observed. The study examines the effects of micro-basin water harvesting and agricultural irrigation on soil moisture dynamics and plant vegetative growth. The soils in the experimental area are colluvial, with a 5 per cent slope, a light texture and a stoniness of 30–55 per cent, and have low water-holding capacity. In the study, four different irrigation levels were tested on 8-year-old olive trees located in two separate plots—one where water harvesting was applied and one where it was not—using a randomized block design. These were: S1 (100 per cent), irrigated to field capacity; S2, irrigated to 70 per cent of field capacity; S3, irrigated to 40 per cent of field capacity; and S4 (0 per cent), which was not irrigated. Based on the results of the ongoing trials over the years, it has been observed that water harvesting practices during arid and semi-arid periods have a positive impact on soil moisture conservation and plant growth. Furthermore, during the 2025 growing season, when the region experienced normal rainfall conditions (>1000 mm), this led to differing growth patterns among the olive sub-groups subjected to water harvesting or not, and those under different irrigation levels. According to the findings, water harvesting practices were effective not only in terms of water-holding capacity but also in relation to hydrological parameters associated with rainfall intensity and duration. Water harvesting is a practice whose positive effects increase over the long term. In the Mediterranean basin, which is subject to climatic variability, this practice helps to safeguard fruit production by facilitating adaptation to change. For this reason, water harvesting is a practice that can be recommended for arid and semi-arid areas.

Keywords: Micro-catchment water harvesting, Olive (*Olea europaea* L.), Drought, Catchment Management, Irrigation.

Acknowledgment: This study was supported by the project titled "Effect of Micro-Catchment Water Harvesting Tecnique on Olive Irrigation," which is carried out by the International Agricultural Research and Training Center of the Türkiye Ministry of Food, Agriculture and Livestock.

Symposium 3- Recent floristic studies in Mediterranean countries

3.1 Gianniantonio Domina - Assessing floristic knowledge advancement in Italy from 1978 to 2025

3.2 Florian Mombrial - Floristic data integration and chorological updates in North Africa: Insights from eFloraMaghreb

3.3 Giacomo Calvia - The vascular flora of the La Maddalena Archipelago (Sardinia): Patterns of change through

3.4 Antoni Buira - Exploring the Iberian flora: Patterns of species discovery, diversity and endemism

3.5 Marco D'Antraccoli - Applying next generation floristics to a Mediterranean protected area: The case of the Migliarino–San Rossore–Massaciuccoli Regional Park (Tuscany, central Italy)

3.6 Abdelmonaim Homrani Bakali - Floristic research in Morocco: Recent discoveries, updated statistics and future directions

3.7 Bahar Gürdal - Floristic studies in the Mediterranean basin of Türkiye

3.1

Assessing floristic knowledge advancement in Italy from 1978 to 2025

Gianniantonio Domina, Gianluigi Bacchetta, Fabrizio Bartolucci, Marco D'Antraccoli, Lorenzo Peruzzi, Adriano Stinca, Alessandro Alessandrini, Liliana Bernardo, Francesco Boscutti, Daniela Bouvet, Maurizio Bovio, Giacomo Calvia, Salvatore Cambria, Fabio Conti, Davide Dagnino, Emanuele Del Guacchio, Gabriele Galasso, Daniela Gigante, Emilio Di Gristina, Simonetta Fascetti, Francesco Falcinelli, Paola Fortini, Domenico Gargano, Leonardo Gubellini, Duilio Iamonico, Mauro Iberite, Daniela Longo, Fernando Lucchese, Andrea Mainetti, Rizzieri Masin, Pietro Medagli, Simone Orsenigo, Enrico Vito Perrino, Lina Podda, Filippo Prosser, Lara Assunta Quaglini, Leonardo Rosati, Annalisa Santangelo, Anna Scoppola, Alberto Selvaggi, Giovanni Spampinato, Sandro Strumia, Federico Maria Tardella, Alessio Turco, Mariacristina Villani, Thomas Wilhalm, Giulio Barone

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This study presents a comprehensive update to the floristic knowledge map of Italy, based on the evaluation of 3,902 local references published between 2005 and 2025, comparing our findings with the previous editions of 1978 [1] and 2005 [2]. We introduce the 'Index of Floristic Knowledge Advancement' (IFA), a quantitative metric that categorizes administrative regions according to the proportion of potential improvement actually achieved over two decades.
Our results demonstrate substantial progress compared to previous assessments. At the national scale, the IFA was 0.22 (limited) when comparing 1978–2005, but increased to 0.30 (moderate) for 2005–2025, indicating an acceleration in floristic documentation. *The most remarkable advancement occurred in Emilia-Romagna, where well-known areas (Level 5) rose dramatically from 26.52% in 2005 to 82.01% in 2025*—an increase of over 55 percentage points. Lombardia, Veneto, and Trentino-Alto Adige also showed substantial gains, confirming the effectiveness of systematic mapping projects and coordinated institutional efforts. A clear widening north-south divide emerges from our diachronic analysis. While northern regions achieved significant progress, Southern Italy and the islands showed near-stagnation, with Calabria and Sicilia exhibiting minimal advancement into higher knowledge categories. Virtually unknown areas (Level 1) have consistently declined across all editions, while fairly well-known (Level 4) and well-known areas (Level 5) demonstrate marked increases—particularly between 2005 and 2025—reflecting the accelerated impact of collaborative initiatives, citizen science, digital databases, and increased taxonomic research focus. Over the past twenty years, 453 new taxa have been described, mostly Italian endemics (443), with *Hieracium* (147 taxa) as the most represented genus. Despite overall progress, 75% of published studies remain geographically restricted, underscoring the need for broader collaborative syntheses to achieve a nationally comprehensive understanding of Italy's exceptional plant diversity.

Keywords: Checklist, Vascular flora, Italian peninsula, Sardinia, Sicily

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3.2

Floristic data integration and chorological updates in North Africa: Insights from eFloraMaghreb

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The Maghreb holds one of the most botanically rich and threatened floras in the Mediterranean Basin, yet systematic knowledge of its distribution and conservation status contains significant gaps. Building on the foundational synonymic and chorological synthesis of DOBIGNARD and CHATELAIN (2011–2013), we developed eFloraMaghreb (efloramaghreb.org), an online platform designed particularly to support herbarium collection management and to improve knowledge of species distribution. The platform currently integrates nearly 104,000 georeferenced herbarium records, representing more than 9,000 species from Morocco, Algeria, and Tunisia, combining both historical collections with recently collected field material. It provides a preliminary assessment of species rarity in the Maghreb and helps identify critical taxa or those requiring further evaluation.

Spatial analyses of this dataset have enabled us to revise species occurrences at the country level and to highlight numerous chorological additions compared with the published synonymic index: approximately 80 taxa represent chorological additions for Morocco and 80 for Algeria, some of which still require confirmation. For endemic taxa, we calculated standard IUCN range metrics (EOO and AOO) to identify taxa with restricted distributions and to prioritize them for formal assessment. We present selected case studies illustrating how the integration of historical collections, georeferenced occurrence data, and recent fieldwork can rediscover taxa unrecorded for decades, clarify distributional uncertainties, and guide survey efforts toward data-deficient regions. Together, these outputs provide the quantitative and cartographic foundation for the development of a regional Red List of the Maghreb flora, an essential conservation tool for this globally significant biodiversity hotspot.

Keywords: Floristic Diversity; Chorology; Endemism; Maghreb Flora; IUCN Red List; Herbarium Informatics

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[2] https://efloramaghreb.org. online database for North African flora

3.3

The vascular flora of the La Maddalena Archipelago (Sardinia): patterns of change through Time

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The La Maddalena Archipelago is located off the Sardinian north-eastern coast and comprises approximately 30 islands and islets. Most are either uninhabited or occupied only seasonally, while the town of La Maddalena hosts about 10,000 inhabitants. Since 1994, the entire archipelago has been included within the La Maddalena National Park. Botanical investigations in the archipelago started in 1870 [1], followed by several floristic studies during the second half of the twentieth century, and a comprehensive vegetation survey in 2005 [2]. Over the last three decades, the archipelago has undergone substantial environmental and socio-economic changes. Traditional activities such as agriculture and livestock farming have progressively declined, while several islands or parts thereof have been designated as strictly protected areas. Meanwhile, tourism pressure has increased considerably, reaching alarming levels during summer and affecting coastal ecosystems. Climate change represents an additional challenge, with prolonged droughts and increasingly extreme temperatures exerting significant stress on wetlands and chasmophytic vegetation. To update floristic knowledge and asses these changes, a detailed survey was conducted over the last three years, supported by a critical review of the available literature. The updated flora currently includes 827 *taxa*, of which 53 are endemic (6.4% of the total flora) and 164 alien (19.8%). Alien component comprises 141 neophytes and 23 archaeophytes, 22 of which are currently invasive within the archipelago. Of the 163 *taxa* first recorded in the archipelago, 67 are native and 96 alien. The native *Elatine brochonii* was first recorded in Italy, whereas 13 alien *taxa* are new to Sardinia and nine to Italy. Endemic, rare, threatened, and phytogeographically significant *taxa* were mapped, and germplasm was collected and preserved *ex situ* in the Sardinian Germplasm Bank (BG-SAR). *In situ* conservation measures were also developed for threatened and European protected species such as *Limonium strictissimum*.

Keywords: Alien taxa, Checklist, Endemic taxa, Mediterranean Basin, Native taxa

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[1] Gennari P., 1870. Florula di Caprera. Nuovo Giorn. Bot. Ital. 2: 90-145
[2] Biondi E., Bagella S., 2005. Vegetazione e paesaggio vegetale dell'arcipelago di La Maddalena (Sardegna nordorientale). Fitosociologia, 42 (2) suppl. 1: 3- 99.

Acknowledgments: Our research is financed by the project "Attività di monitoraggio, conservazione e raccolta del germoplasma della flora vascolare nel Parco Nazionale dell'Arcipelago di La Maddalena", funded by the National Park of La Maddalena.

3.4

Exploring the Iberian flora: Patterns of species discovery, diversity and endemism

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The Iberian Peninsula is one of the most species-rich areas within the Mediterranean Basin, harbouring approximately 6,900 native taxa, about one quarter of which are endemic. The completion of *Flora iberica*, together with the increasing availability of distributional and phylogenetic data, provides an opportunity to assess our knowledge of the Iberian vascular flora and explore the spatial and environmental patterns underlying its diversity.

The history of species description since 1753 reveals two major peaks of discovery in the Iberian endemic flora, associated with botanical exploration during the mid-nineteenth century and with renewed taxonomic activity during the late twentieth century, particularly within the framework of *Flora iberica*. Although the rate of discovery has progressively declined, the inventory remains incomplete, particularly for range-restricted species.

Comparisons between the native and endemic floras in their taxonomic composition, life forms and ecological preferences provide insights into the distinctive features of Iberian endemism. Spatial analyses reveal marked geographical patterns in both overall species richness and endemic richness, although the influence of sampling intensity varies among diversity metrics. Mountain systems are particularly important centres of plant diversity, with the Baetic ranges standing out as the main centre of Iberian endemism.

The incorporation of phylogenetic information provides an evolutionary perspective on these patterns. Analyses of phylogenetic endemism and its environmental correlates highlight the combined effects of climate, topography and soil, with edaphic factors playing a particularly important role in explaining patterns of recent diversification.

Keywords: Iberian Peninsula; Endemic flora; Species discovery; Species richness; Phylogenetic endemism

Acknowledgment: Projects DAHPNE (ref. PID2024-158450NB-I00), funded by MCIN/AEI/10.13039/501100011033/ERDF, EU and HISPAPHYLO (ref. PID2021-124234NA-I00)

3.5

Applying next generation floristics to a Mediterranean protected area: The case of the Migliarino–San Rossore–Massaciuccoli Regional Park (Tuscany, central Italy)

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Floristic inventories are a fundamental output of systematic botany, but their compilation is often methodologically heterogeneous, weakly standardised and only partly reproducible. Following the workflow proposed for Next Generation Floristics [1], this contribution uses the vascular flora of the Migliarino–San Rossore–Massaciuccoli Regional Park (Tuscany, central Italy) as a case study to assess how quantitative and data-integrative tools can strengthen floristic research. The Park is a large coastal protected area encompassing a marked environmental mosaic of dunes, wetlands, freshwater and brackish habitats, pinewoods, woodlands ranging from hygrophilous to xerophilous types, grasslands, and agricultural landscapes. The workflow combines three complementary methodological approaches. First, Species–Area Relationship models are used to estimate the expected number of taxa in the study area [2], providing an explicit benchmark for evaluating sampling completeness and floristic richness. Second, Maps of Relative Floristic Ignorance are produced to visualise the spatial distribution of knowledge gaps, transform uncertainty into an operational variable, and identify priority areas for further investigation. Third, optimised sampling procedures are applied to improve the spatial and environmental allocation of field effort. To support field surveys, we also propose an R-based multi-objective sampling optimisation routine that identifies a user-defined number of target sampling units while jointly considering spatial configuration, environmental heterogeneity, and floristic ignorance. The data-collation phase combines records derived from traditional bibliographic and herbarium sources with validated occurrence data from online biodiversity resources, such as GBIF, iNaturalist and the Italian national platform Wikiplantbase. The field phase combines probabilistic and purposive sampling, thereby balancing reproducibility and spatial explicitness with the efficiency of expert botanical exploration. This case study shows how the resulting floristic inventory can move beyond descriptive compilation and become an analytically robust, transparent, and updatable research infrastructure for contemporary systematic botany.

Keywords: Next Generation Floristics, Floristic inventory, Sampling optimisation, Species–Area Relationship, Maps of Relative Floristic Ignorance

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3.6

Floristic research in Morocco: Recent discoveries, updated statistics and future directions

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Floristic research in Morocco has accelerated significantly over the past decade, consolidating the country as one of the principal centres of plant diversity in the Mediterranean Basin. The present study provides a comprehensive update of the Moroccan Angiosperm checklist, integrating recent taxonomic and nomenclatural studies. The updated checklist comprises 5,959 taxa distributed among 150 families and 1,173 genera, confirming the exceptional richness and complexity of the Moroccan flora. Asteraceae, Fabaceae, and Poaceae remain the most species-rich families, while *Silene*, *Ononis*, *Centaurea*, and *Euphorbia* are the largest genera.

Endemism continues to be one of the defining characteristics of the flora. Approximately one-third of all accepted taxa are endemic in the broad sense, including a remarkable proportion of strict Moroccan endemics (~16%), while numerous taxa are shared with the Iberian Peninsula, Algeria and the Canary Islands. These distributions highlight Morocco as a major biogeographic crossroads where Mediterranean, Macaronesian, Atlantic, Saharo-Arabian, and Irano-Turanian floristic elements converge. Nevertheless, hundreds of taxa remain of uncertain presence, emphasizing the need for continued field exploration, herbarium revision, and taxonomic reassessment.

The Moroccan flora continues to expand through the discovery of new taxa, new national records, nomenclatural revisions, and improved distributional knowledge. Recent taxonomic activity has been particularly intense, with more than 180 newly published taxa and/or nomenclatural modifications between 2015 and 2025, reflecting renewed botanical exploration and systematic research. Despite this progress, integrative systematic studies combining molecular phylogenetics with morphology, ecology, and biogeography remain available for only a limited number of Moroccan plant groups, leaving several taxonomically complex genera insufficiently resolved.

This presentation provides the first comprehensive statistical synthesis of the updated Moroccan Angiosperm checklist, including taxonomic diversity, endemism, some chorological patterns, conservation status, and recent floristic advances. The results establish an updated baseline for future taxonomic, biogeographic and conservation research and reinforce Morocco's importance as one of the foremost centres of vascular plant diversity and endemism in the Mediterranean region.

Keywords: Angiosperms; Moroccan flora; Endemism; IUCN conservation status; Floristic checklist; Mediterranean biodiversity; New taxa; Taxonomic revision; Fennane 2021

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3.7

Floristic studies in the Mediterranean basin of Türkiye

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The Mediterranean Basin is globally recognized as a biodiversity hotspot due to its exceptional species richness and high levels of endemism.

Türkiye occupies a unique biogeographical position at the intersection of three phytogeographical regions: Mediterranean, Irano-Turanian, Euro-Siberian. This intersection significantly enhances its floristic complexity. Floristic studies in Türkiye have a long tradition, with foundational works such as "Flora of Türkiye and the East Aegean Islands" providing a taxonomic backbone. Following the publication of the Flora of Türkiye (1965-2000), floristic studies has greatly increased, resulting in the addition of numerous new taxa to the flora of Türkiye. From 2000 to 2025, 1385 new taxa have been described from Türkiye, highlighting the country's ongoing floristic richness and taxonomic potential [1, 2]. Notably, approximately 25% of these taxa originate from the Mediterranean Basin, emphasizing its role as a major center of recent speciation and discovery. The classification of these newly described taxa reveals a strong dominance of dicotyledons (64.7%), followed by monocotyledons (35%), with gymnosperms represented by three taxa. Family-level distribution indicates that speciation and taxonomic discovery are not evenly distributed. Instead, certain families show remarkable prominence, particularly Iridaceae and Liliaceae, both of which are strongly associated with geophytic life forms and Mediterranean climatic adaptations. Other families with significant contributions include Asteraceae, Brassicaceae, Apiaceae, and Lamiaceae, which are known for their ecological plasticity and high diversification rates in Mediterranean-type ecosystems.

The Mediterranean Basin is the source of 14% of the new records that have been added to the flora of Türkiye. Despite its richness, the Mediterranean flora of Türkiye faces significant threats: urbanization, agricultural expansion, tourism development, climate change. Conservation efforts should prioritize endemic-rich areas.

In conclusion, the Mediterranean Basin of Türkiye represents an important center of plant diversity, and floristic studies remain essential for both scientific understanding and biodiversity conservation.

Keywords: Additional Taxa, Floristic Studies, Mediterranean Basin, New Taxa, Türkiye

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[2] Özhatay, N. et al., *İstanbul Journal of Pharmacy*, 2019, 49(2), 105-120

Symposium 4- Chemical diversity of medicinal and aromatic plants and their health benefits

Chairs: İhsan Çalış, Müberra Koşar

4.1 Funda Nuray Yalçın - Secondary metabolites targeting urological cancers

4.2 F. Sezer Senol Deniz - Evaluation of the effects of some plants from the Lamiaceae family grown in Türkiye against Alzheimer's Disease by *in vitro* and *in vivo* methods

4.3 Burçin Karakuzu - Phytochemical studies on the leaves of *Astragalus tmoleus* var. *bounacanthus* and investigation of their effects on cellular senescence

4.4 Ilgaz Akata - From poison to potential: A review of the toxic mushrooms of Türkiye

4.5 Golshan Zare - Metabolomic profiling- based chemotaxonomic evaluation of the genus *Iberis* (Brassicaceae) in Türkiye

4.6 İhsan Çalış - Exploring the chemical diversity of Mediterranean plants: New natural products and recent findings from our research

4.7 Tuğba Subaş - Investigation of the skin-related enzyme inhibitory, antioxidant activity and phenolic profile of *Satureja spicigera*

4.1

Secondary metabolites targeting urological cancers

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In urogenital cancers (including the kidney, bladder, prostate, and testis cancers), limitations of current treatment options, significant side effects, and high costs often contribute to treatment failure. Consequently, efforts to increase survival rates, reduce treatment expenses, and provide optimal therapies with maximal benefit and minimal adverse effects have led to increased interest in natural products [1-2]. Secondary metabolites derived from plants have long been observed to influence cancer progression [3]. Among these, phenolic compounds, flavonoids, and terpenes are the primary molecules responsible for anticancer effects. These secondary metabolites have demonstrated antiproliferative, antitumoral, apoptotic, and antimetastatic activities against cancer cells through various mechanisms [4]. Numerous clinical trials are currently investigating the therapeutic profiles, side effects, and properties of natural products with potential applications in urogenital cancers.

Keywords: Secondary metabolites, Urogenital cancers

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4.2

Evaluation of the effects of some plants from the Lamiaceae family grown in Türkiye against Alzheimer's Disease by *in vitro* and *in vivo* methods

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Alzheimer's disease (AD) is a progressive neurodegenerative disorder with no definitive cure. Current cholinesterase inhibitors and N-methyl-D-aspartate (NMDA) antagonists provide only symptomatic relief [1], highlighting the need for therapeutic strategies targeting the underlying mechanisms of AD, including amyloid accumulation, tau pathology, oxidative stress, and neuroinflammation. The clinical success of galantamine, a natural alkaloid from *Galanthus nivalis* L., underscores the potential of natural products in AD drug discovery. The Lamiaceae family represents an important resource for neuroprotective research, as it includes the genus *Salvia* sp. (sage), which is known in traditional medicine for its memory-enhancing effects [2]. Based on this information, the *in vitro* activities against AD-related enzymes [acetylcholinesterase (AChE), butyrylcholinesterase (BChE), β-secretase (BACE-1), protein tyrosine phosphatase 1B (PTP1B), prolyl oligopeptidase (POP)] and anti-neuroinflammatory effects using SH-SY5Y cells of dichloromethane, ethyl acetate, and ethanolic extracts of eight taxa belonging to the genera *Lavandula*, *Leonurus*, and the scarcely studied *Chaiturus* growing in Türkiye were investigated. Activity-guided fractionation of the dichloromethane extract of *Lavandula stoechas* subsp. *stoechas*, which exhibited activity through multiple mechanisms, was performed by monitoring BChE inhibition. GC-MS and LC-MS analyses were used to characterize the active constituents of the extract and fractions. Ursolic acid was identified as a major compound in both the crude extract and active fraction (270.03 and 36.31 mg/g, respectively). The possible interactions of ursolic acid with the enzymes were examined using *in silico* methods. The *in vivo* effects of the active extract, fraction, and ursolic acid were subsequently evaluated in a scopolamine-induced amnesia model in rats using behavioral tests, histopathological evaluation, and immunohistochemical analyses. The findings demonstrated promising neuroprotective effects of the crude extract, active fraction, and ursolic acid, supporting L. *stoechas* subsp. *stoechas* as a potential natural source for developing novel therapeutic strategies against AD.

Keywords: Alzheimer's disease, Anti-neuroinflammatory activity, *In vivo* amnesia model, ursolic acid, *Lavandula stoechas* subsp. *Stoechas*

References:

[1] Godyń, J. et al. *Pharmacological Reports*, 2016, 68(1), 127-138.
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4.3

Phytochemical studies on the leaves of *Astragalus tmoleus* var. *bounacanthus* and investigation of their effects on cellular senescence

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Astragalus is the largest genus in the family Leguminosae and is widely distributed throughout the temperate region of the world and has been traditionally used to treat diabetes, nephritis, and uterine cancer [1]. *Astragalus* species have rich secondary metabolite content, including triterpene saponins, flavonoids, and phenolic compounds, and these metabolites exhibit antioxidant, anti-inflammatory, immunostimulant, and anti-aging effects [1,4]. Considering these facts, especially their significant activities versus aging and age-related disorders [4], we have initiated a study aiming to isolate secondary metabolites from leaves of *Astragalus tmoleus* var. *bounacanthus* (Boiss.) D. F. Chamb (ATL), an endemic species to Türkiye, and their bioactivities on senescence markers at cellular level.
Air-dried leaves of ATL were extracted with methanol under reflux, and the crude extract (ATLE) was fractionated on resin column, followed by further chromatographic isolation steps using different stationary and mobile phases. As a result, 11 compounds were isolated, and structures of the isolates were established through comprehensive spectroscopic analyses [IR, 1D- and 2D- NMR, HRESIMS]. The isolates comprised cycloartane- and oleanane-type triterpenes, amino acid conjugates, flavonol glycosides, and a lignan. Among them, five were characterized as new natural products, representing the first phytochemical investigation of this endemic species. The anti-senescent potential of ATLE and the isolated compounds was evaluated in a doxorubicin-induced senescent human dermal fibroblast adult (HDFa) cell model. Cellular senescence was assessed by measuring p21 mRNA expression and intracellular reactive oxygen species (ROS) accumulation. The results revealed that ATLE and four compounds significantly downregulated p21 mRNA expression and reduced intracellular ROS levels. These findings suggest that the extract and the active molecules may possess senoreverter-like potential by partially reversing the senescent phenotype. Overall, leaves of *A. tmoleus* var. *bounacanthus* represent a sustainable source of structurally diverse bioactive metabolites with promising anti-senescent potential.

Keywords: *Astragalus*, Secondary Metabolites, Saponin, Phenolics, Cellular Senescence

References:

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Acknowledgment: This work was supported by TÜBİTAK (Project No. 125Z064), with technical infrastructure and equipment provided by NMRM and BIYOMER.

4.4

From poison to potential: A review of the toxic mushrooms of Türkiye

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Türkiye hosts a rich diversity of poisonous mushrooms and their chemically diverse metabolites, which pose a public health risk and represent a largely underexplored source of pharmacologically active natural products. This literature-based review synthesizes published records of poisonous mushrooms reported from Türkiye up to March 2026, with emphasis on taxonomic diversity, geographic occurrence, principal toxins, toxicological mechanisms, and potential biomedical relevance. The review documents 77 species classified as poisonous, while 101 additional taxa are treated as potentially poisonous, doubtfully harmful, or mainly associated with gastrointestinal disorders. Major metabolite classes include amatoxins, phallotoxins, virotoxins, gyromitrin, orellanine, muscarine, coprine, isoxazoles, tryptamines, illudins, gymnopilins, and bolesatine. These compounds produce effects ranging from gastrointestinal and cholinergic syndromes to neurotoxicity, hepatotoxicity, nephrotoxicity, and fatal multi-organ damage. Rather than considering these taxa exclusively as causes of intoxication, this review evaluates poisonous mushrooms as sources of structurally diverse fungal metabolites relevant to toxicology, pharmacology, and natural-product research. Particular attention is given to relationships among toxin classes, target organs, symptom onset, and associated clinical syndromes, as well as to uncertainties concerning species identification, toxin attribution, and geographic documentation. Because many published records are based primarily on morphological identification and chemical or molecular confirmation is unavailable for numerous taxa, the current inventory should be interpreted as a critical synthesis of the available literature rather than a fully validated toxicological checklist. The review also identifies major research priorities, including reassessing historical collections, standardizing taxonomic nomenclature, verifying species–toxin associations, and expanding regional toxicological surveillance. Integrating contemporary taxonomy, targeted metabolite profiling, and clinical toxicology will be essential for improving risk assessment, strengthening public health awareness, and identifying fungal metabolites worthy of further biomedical investigation.

Keywords: Fungal toxins; Natural products; Poisonous mushrooms; Public health; Türkiye

4.5

Metabolomic profiling-based chemotaxonomic evaluation of the Genus *Iberis* (Brassicaceae) in Türkiye

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The genus *Iberis* L. (Brassicaceae) is mainly distributed across the Mediterranean Basin, with Europe representing its primary center of diversity. In Türkiye, the genus is represented by ten taxa, including four endemic taxa [1]. Although the genus has been investigated in terms of morphology and molecular phylogeny, its comprehensive metabolomic and phytochemical diversity remains insufficiently explored [2]. In the present study, plant materials previously used in morphological and molecular analyses were subjected to LC-MS-based untargeted metabolomic profiling in order to investigate chemotaxonomic relationships among Turkish *Iberis* taxa. This integrated approach enabled a direct comparison between metabolite patterns and existing taxonomic frameworks derived from classical and molecular data [3].

A total of 149 LC–MS features were putatively annotated. Primary metabolites showed high conservation across taxa, whereas secondary metabolites displayed significant interspecific variation. Multivariate statistical analyses, including clustering and ordination methods, revealed clear grouping patterns that were largely consistent with previously established morphological and molecular phylogenetic relationships. In particular,*Iberis sempervirens*, *I. saxatilis*, and*I. Odorata* formed well-supported and distinct clusters, while the metabolite profiles also reflected the internal structure of the *I. simplex* complex, supporting its taxonomic complexity. Overall, this study provides the first comprehensive metabolomic assessment of Turkish *Iberis* taxa and demonstrates that LC-MS-based untargeted metabolomic profiling is a powerful and reliable tool for resolving taxonomic relationships.

Keywords: Chemotaxonomy, *Iberis,* Metabolomics, Phytochemicals, Türkiye
References:

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4.6

Exploring the chemical diversity of Mediterranean plants: New natural products and recent findings from our research

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Natural products remain a major source of structurally diverse molecules for drug discovery. In addition to microorganisms, fungi, and marine organisms, terrestrial plants have long been among the principal subjects of natural-product research because they are comparatively accessible and can generally be identified and documented with taxonomic precision.

Our continuing investigations of plants from the flora of Türkiye and other parts of the Mediterranean Basin have resulted in the isolation and structural characterization of numerous classes of secondary metabolites. The plant species investigated were selected based on chemotaxonomic, ethnopharmacological, and phylogenetic considerations, as well as through exploratory phytochemical screening.

This presentation will focus on selected members of the Lamiaceae, including species of *Phlomis* L. [1] and *Teucrium* L. [2,3]; Asteraceae, represented by *Rhaponticum acaule* (L.) DC.; Primulaceae, represented by species of *Cyclamen* L.; Polygalaceae, represented by species of *Polygala* L.; and Fabaceae, represented by species of *Astragalus* L. The investigated plants were collected from the floras of Türkiye and Libya.

These studies led to the isolation of structurally diverse natural products, including iridoids, phenylethanoid glycosides, flavonoids, xanthones, oligosaccharide multiesters, ecdysteroids, oleanane- and 13β,28-epoxyoleanane-type saponins, and cycloartane-type triterpene glycosides. The structures of the isolated compounds were elucidated using various chromatographic methods, spectroscopic techniques, including UV, IR, one- and two-dimensional NMR spectroscopy and high-resolution mass spectrometry, and, where necessary, chemical derivatization.

A considerable number of previously undescribed natural products were characterized during these investigations. The principal themes emerging from this research include the discovery of new natural products, the elucidation of complex molecular structures, the evaluation of their chemotaxonomic significance, and the investigation of their potential biological relevance.

This presentation will provide an overview of these recent findings and illustrate the remarkable chemical diversity of selected Mediterranean plants.

Keywords: Asteraceae, Lamiaceae, Fabaceae, Polygalaceae, Primulaceae

References:

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4.7

Investigation of the skin-related enzyme inhibitory, antioxidant activity and phenolic profile of *Satureja spicigera*

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Global interest in and demand for cosmetic products is increasing steadily. Owing to their secondary metabolites, plants constitute important natural sources for the development of dermocosmetic products [1]. *Satureja* species (Lamiaceae) are used both as food and for medicinal purposes in the treatment of ailments such as nausea, diarrhea, cramps, and indigestion [2]. This study aimed to evaluate the potential dermocosmetic applicability of the aerial parts (leaves and stems) of *S. spicigera* and to determine its phenolic profile. The collagenase and tyrosinase inhibitory activities of the methanol extract, along with its chloroform, ethyl acetate, and remaining aqueous subextracts, prepared from the species, were evaluated spectrophotometrically, and their antioxidant activity was assessed using the $ABTS^{\bullet+}$ (2,2-azino-bis-3-ethylbenzothiazoline-6-sulphonic acid) radical scavenging assay. The phenolic profile of the extracts was investigated using high-performance liquid chromatography (HPLC). Although the extracts exhibited weaker enzyme inhibitory activity compared with the positive controls (catechin, kojic acid), the ethyl acetate subextract was found to be more effective than the other extracts (IC_{50} for collagenase: 40.786 ± 0.874 µg/mL; for tyrosinase: 51.328 ± 2.705 µg/mL). The ethyl acetate subextract also showed the highest $ABTS^{\bullet+}$ radical scavenging capacity (559.294 ± 6.487 µM). Among the phenolic compounds of the ethyl acetate subextract, rosmarinic acid (441.576 ppm), vanillic acid (7.4544 ppm), *p*-coumaric acid (5.6264 ppm), and *p*-hydroxybenzoic acid (4.6048 ppm) were identified as the major constituents. It was determined that *S. spicigera*, and particularly its ethyl acetate subextract, shows potential as a natural raw material for dermocosmetic products; however, further studies are required.

Keywords: Lamiaceae, Collagenase, Tyrosinase, ABTS, HPLC

References:

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Symposium 5- Integrative taxonomy

Chairs: Musa Doğan, Božo Frajman

5.1 Martina Temunovic - Combining genomic data with ecological niches informs taxonomy within *Dianthus ciliatus* and *D. sylvestris*

5.2 Cyllène Chatellier - Biogeography as a formal condition for species delimitation: A case study in Mediterranean *Romulea* (Iridaceae)

5.3 Lorenzo Peruzzi - TOI (Turrill's Omega Index) a new heuristic index for quantifying the support of a taxonomic hypothesis

5.4 Božo Frajman - Integrative approach in resolving taxonomy and diversification of the Mediterranean *Euphorbia* (Euphorbiaceae)

5.5 Marek Slovak - The legacy of historical hybridisation and introgression in Mediterranean endemic speciation: Insights from the genera *Daphne* (Thymelaeaceae) and *Picris* (Compositae)

5.6 Maria-Anna Vasile - Integrative taxonomy of Boraginales across scales: Resolving relationships from global family-level patterns to species-level diversification in Mediterranean radiations

5.7 Emine Akalın - Integrative taxonomy and recent systematic revisions of species-rich Apiaceae genera in Türkiye

5.1

Combining genomic data with ecological niches informs taxonomy within *Dianthus ciliatus* and *D. sylvestris* (Caryophyllaceae)

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Dianthus (Caryophyllaceae) is one of the most diverse plant genera in the Mediterranean, where rapid diversification has been driven by the interplay between Quaternary climatic fluctuations and genome evolution. Here, we investigate how past and current climate and polyploidisation have shaped genomic variation, ecological differentiation, and distribution patterns in two *Dianthus* species complexes. The *D. sylvestris* complex comprises a large number of taxa, initially identified based on morphology. However, recently revealed evolutionary lineages within this complex do not reflect current taxonomy, as species boundaries are primarily determined by past demographic events. In *D. sylvestris* s.l., we combined RAD-seq SNPs, demographic modelling and species distribution models to reconstruct population demographic dynamics and to investigate associations between population genetic and climatic variation across the Balkan Peninsula, a major European glacial macrorefugium. We identified two main genetic groups, with hierarchically nested population phylogeographic structure suggesting further microrefugia within the Balkan macrorefugium. Population genetic variation was significantly associated with geography and current climate.

In *D. ciliatus* s.l., we investigated the relationship between polyploidisation and niche evolution in relation to the intraspecific taxonomy of this amphi-Adriatic endemic, which comprises three recognised subspecies. We identified two ploidies: diploids were restricted to the Balkan Peninsula, whereas more widespread tetraploids occupied a broader amphi-Adriatic distribution. We also found significant differences in relative genome size (RGS), corresponding to the current taxonomy. Niche comparisons revealed low pairwise overlap, with each subspecies-ploidy combination occupying distinct environmental niches. Significant niche conservatism between diploid and tetraploid *D. ciliatus* subsp. *ciliatus* suggests an autopolyploid origin of these tetraploids. Overall, broader tetraploid niches likely facilitated their dispersal into novel environments and their expansion to the Apennine Peninsula. Together, our results demonstrate that past climate-driven demographic processes and polyploidisation have both played important roles in shaping the genetic, ecological and taxonomic diversity of Mediterranean *Dianthus*.

Keywords: Niche evolution, Population genetics, Refugia, Taxonomy, Ecology

Acknowledgment: (This work was supported by Croatian Science Foundation project AmphiAdriPlant (UIP-2017-05-2882) and by the Austria–Croatia bilateral project "Genome size evolution and polyploidization in amphi-Adriatic *Aurinia* (Brassicaceae) and the *Cerastium tomentosum* and *Dianthus sylvestris* species groups (Caryophyllaceae)" (HR17/2020) funded by the Austrian Agency for International Cooperation and the Croatian Ministry of Science and Education.)

5.2

Biogeography as a formal condition for species delimitation: A case study in Mediterranean *Romulea* (Iridaceae)

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Under the unified species concept (USC), species are defined as independently evolving metapopulation lineages, with classical criteria (distinct morphology, reproductive isolation, monophyly, genetic clustering) serving as lines of evidence. However, these signals frequently conflict in recently diverged taxa, requiring an explicit spatial and historical framework to guide interpretation. Here, we demonstrate how integrating a biogeographic approach operationalizes species delimitation under the USC, using a taxonomically ambiguous plant genus.

We focus on two taxa of the *Romulea* genus (Iridaceae) in the Mediterranean region: *R. florentii* Moret, endemic to the Hyères archipelago (Provence, France), and *R. requienii* Parl., from Corsica and Sardinia. Despite morphological similarity and weak genomic divergence reported previously, their lineage independence remains untested. We sampled their full distribution range using Angiosperms353 target capture, leveraging paralog-aware species tree inference, divergence dating, ploidy assessment, population genetic structure analyses, and demographic modelling.

Genomic analyses reveal robust differentiation between the Provençal and Corso-Sardinian taxa (FST = 0.23–0.25), with divergence in the early Pleistocene, approximately 2.3 Ma (95% HPD: 1.60–3.14 Ma). These ancient split supports lineage independence, yet demographic simulations uncover low contemporary bidirectional migration between Provence and Corsica ($m = 5.4–6.6 \times 10^{-5}$ per generation). This incomplete separation is mirrored by a clinal ancestry gradient across Corsica, where northern populations exhibit Provençal–Sardinian signatures, indicating a localized secondary contact zone.

Crucially, this structured admixture is only interpretable within the biogeography of the western Mediterranean (Tyrrhenian area). By pairing full-distribution sampling with demographic simulations, we disentangled historical ancestral polymorphism from contemporary gene flow. Our findings show that genomic divergence alone, without genetic structure investigation, can be insufficient to resolve species boundaries. We propose biogeographic context as a foundational framework in integrative species delimitation, structuring the scientific question and sampling strategy, particularly in recently diverged taxa with discordant genomic signals.

Keywords: Species delimitation, Biogeography, Integrative taxonomy, Population genomics, Tyrrhenian area

Acknowledgment: The project was supported by the Port-Cros National Park (convention 2022-593). We thank Virgile Noble and Henri Michaud (Conservatoire Botanique National Méditerranéen) for field collection in Provence, Daniel Pavon (IMBE) for additional sampling, Alain Delage and Lisandru Leandri (Conservatoire Botanique de Corse) for collection in Corsica. Andrea Lallai, and Gianluca Iiriti are thanked for sampling in Sardinia. We are grateful to Anouar Toumi (IMBE) for his contribution to bioinformatic pipeline development.

5.3

TOI (Turrill's Omega Index) a new heuristic index for Quantifying the Support of a taxonomic hypothesis

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Biological research relies on the use of taxa, expressed in the form of a Latin binomial for species. Taxa are commonly considered proven, however they represent hypotheses on the distribution of natural biological variation that can change their status when new systematic knowledge is produced. The long-standing problem affecting systematics and taxonomy, having deep impacts on other biological disciplines, is that the binomial itself does not bring the information concerning its solidity as a hypothesis. We developed a standardized heuristic index, named Turrill's Omega Index (TOI), that allows to estimate the degree of support of a taxonomic hypothesis. TOI is a single number, calculated from the integration of four macro-categories of comparative data concerning Phenotype, Genealogy, Isolation, and Geography-Ecology. TOI provides a practical and reliable solution to quantify the support of a taxonomic hypothesis, avoiding the long-standing debate concerning species delimitation and species concepts. In addition, TOI can support conservation decision-making by helping prioritize funding allocation among equally threatened taxa according to their degree of support. In this context, TOI is an additional component to be considered when striving for more informed conservation decisions. As a collaborative pilot project carried out by the Working Group for Floristics, Systematics, and Evolution of the Italian Botanical Society, we selected around 600 species and subspecies endemic to 17 well-defined biogeographical areas in Italy. The project is currently ongoing with bibliographic research and TOI assessments expected to be completed by July and complete the analyses by October 2026. For each biogeographical area, TOI values will be compared with National Red List IUCN assessments to test whether taxa facing the highest extinction risk also correspond to well-supported taxonomic hypotheses.

Keywords: Biodiversity, Species hypothesis, Systematics, Taxonomy

5.4

Integrative approach in resolving taxonomy and diversification of the Mediterranean *Euphorbia* (Euphorbiaceae)

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Euphorbia is with over 2150 species one of the largest genera of flowering plants. Most species occurring in the Mediterranean Basin belong to *Euphorbia* subgenus *Esula*, which comprises roughly 480 species and represents the most significant radiation of the genus in temperate areas of the Old World. We will present the outcomes of past [1, 2] and ongoing studies on diversification of different Mediterranean *Euphorbia* lineages, based on integrative approach. We applied phylogenomic analyses of RAD sequencing data, relative genome size estimations, multivariate morphometrics and environmental niche modelling to disentangle relationships in different lineages of the Mediterranean *Euphorbia.* More specifically, we will present the (1) diversification of the *Euphorbia acanthothamnos* alliance centred in the Eastern Mediterranean, including a description of a new species from the southern margins of the Taurus Mountains in Anatolia, (2) relationships within the central Mediterranean *E. bivonae* group that indicate biogeographic links between southern Italy and northern Africa, (3) diversification of the western Mediterranean *E. pithyusa* group, where multiple long distance dispersals among the western Mediterranean islands and European and African coasts have been inferred, as well as the (4) evolutionary pathways leading to the origin Corsican-Sardinian endemic *E. gayi* as well as *E. variabilis* and *E. valliniana* endemic to the south-western margins of the Alps.

Keywords: Aegean islands, Anatolia, *Euphorbia*, Mediterranean islands, Endemism.

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5.5

The legacy of historical hybridisation and introgression in Mediterranean endemic speciation: Insights from the genera *Daphne* (Thymelaeaceae) and *Picris* (Compositae)

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The Mediterranean Basin is a global biodiversity hotspot with exceptionally high endemism. Its endemic lineages have diversified over long geological timescales through allopatric and ecological speciation, complemented by introgression and whole-genome duplication. Recurrent paleoclimatic and paleogeological oscillations have driven pronounced niche dynamics and the formation of secondary contact zones, promoting gene flow at both homoploid and polyploid levels. Using an integrative framework that combines genomic, karyological, cytogenetic, and ecological data, we investigated the evolution of endemic species in two model genera whose main centres of diversification and species richness lie in the Mediterranean. Endemic speciation via allopolyploidisation is exemplified by *Daphne reichsteinii* (Thymelaeaceae) from the pre-Alpine Lake Garda region at the northern periphery of the Mediterranean. We confirmed its Pleistocene origin, involving the Tertiary-relict endemic *D. petraea* as the paternal parent and an as-yet-unidentified cytotype lineage within the polyploid *D. alpina* complex as the maternal parent. In contrast, homoploid speciation, accompanied by historical introgression shaping eastern Mediterranean endemics, is exemplified by diploid members of the genus *Picris* (Compositae). We detected two major historical introgression events involving the Turkish Tertiary endemic *P. campylocarpa*, which introgressed into the most recent common ancestor (MRCA) of the *P. cyprica–P. pauciflora* lineage and into the MRCA of the B1 subclade (*P. hieracioides* group). Both Turkish/Cyprus endemics, *P. cyprica* and *P. campylocarpa*, harbour cryptic lineages distributed across southern Türkiye and Cyprus, embedded in complex, network-like patterns of introgression that also involve widespread *P. pauciflora*. The evolutionary history of another diploid Turkish endemic, *P. olympica*, is closely linked to Pleistocene Anatolian orogeny and climatic oscillations, facilitating secondary contacts within the species of *P. olympica*. Together, these processes have generated cryptic, likely undescribed endemic taxa that warrant detailed taxonomic, evolutionary, and biogeographic revision.

Keywords: Genomics, Relicts, Pleistocene climatic oscillations

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5.6

Integrative taxonomy of Boraginales across scales: Resolving relationships from global family-level patterns to species-level diversification in Mediterranean radiations

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Boraginales comprise a subcosmopolitan order of approximately 2700 species whose higher-level classification has long remained in flux. Our recently published global phylogeny, sampling >80% of the genera and based on the Angiosperms353 probe set, largely corroborates previously inferred relationships while improving backbone resolution [1]. Combined with long-standing developmental morphological studies, these results suggest that shifts in placentation, ovule number, and stamen–corolla tube modifications are associated with the evolution of major lineages. Based on this integrative evidence, we recognize nine families within Boraginales, a classification now adopted by the Boraginales Taxonomic Expert Network of World Flora Online.

Having established the taxonomic framework at family level, the next challenge is to understand diversification and morphological evolution within species-rich genera of the order. Here, we focus on two predominantly Mediterranean/Tethyan lineages of Lithospermeae (Boraginaceae), *Alkanna* (~ 68 spp.) and *Onosma* (~ 247 spp.), which exhibit the highest species diversification rates in the tribe [2]. Both genera remain taxonomically challenging, with still unclear species boundaries due to high morphological variability and limited phylogenetic sampling so far. This makes them ideal systems to investigate the interplay between rapid diversification, morphological evolution, and biogeography.

To address this, we follow an integrative approach, combining phylogenomics and detailed morphological analyses. We develop a custom probe set for Lithospermeae targeting hundreds of low-copy nuclear genes, enabling phylogenomic analyses at finer taxonomic scales. We are currently assembling a comprehensive sampling across the full distribution range of both genera, using herbarium collections as well as plant material from extensive fieldwork in Greece, one of their endemism centres. Preliminary analyses suggest that several traditionally diagnostic characters (e.g., nutlets, corolla and indumentum) show extensive homoplasy, highlighting the need for an integrative reassessment of species boundaries in both genera.

Keywords: Boraginaceae, Integrative taxonomy, Species delimitation, Micromorphology, Evolution

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5.7

Integrative taxonomy and recent systematic revisions of species-rich Apiaceae genera in Türkiye

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Türkiye, situated at the crossroads of three major phytogeographical regions, represents one of the most significant centres of diversification for the family Apiaceae. The most recent inventory now recognizes 107 genera from Türkiye, a substantial increase from earlier treatments reflecting ongoing generic-level revisions driven by molecular phylogenetic evidence.

This presentation examines recent systematic revisions and biodiversity assessments of selected species-rich genera within subfamily Apioideae, including *Ferulago* s.l., *Ferula, Pimpinella, Bupleurum*, and the *Peucedanum* complex. Nuclear ribosomal ITS/ETS and plastid sequence data have substantially reshaped generic boundaries, revealing that several traditionally recognized groupings are polyphyletic and necessitating major nomenclatural revisions.

The most consequential recent revision concerns *Ferulago* within the *Cachrys* clade. Combined molecular and morphological analyses demonstrated that *Ferulago* is clearly polyphyletic, leading to its division into four genera: *Ferulago* s.s. (monotypic, endemic to Crete), reinstated *Lophosciadium* DC. (40 taxa, centred in Anatolia), elevated *Anisotaenia* (11 species, six in Türkiye), and newly described *Aenigmosciadium* (monotypic, eastern Türkiye) [1]. Significant revisions were also conducted in *Angelica* and *Xanthogalum* within tribe *Selineae*, resulting in the description of new endemic taxa and inter-generic transfers [2]. Parallel revisions reshaped the *Peucedanum* complex into several segregate genera, while *Ferula* was expanded to 27 species through an integrative approach combining morphological, ITS-based phylogenetic, and sesquiterpenoid chemotaxonomic evidence.

Collectively, these findings underscore that Anatolia constitutes an exceptional centre of diversification for multiple Apiaceae lineages, and demonstrate the indispensable role of integrative taxonomy combining molecular, morphological, anatomical, and phytochemical evidence in achieving a stable and predictive classification of the family.

Keywords: Apiaceae, Integrative taxonomy, Molecular phylogenetics, chemotaxonomy, Türkiye

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Symposium 6- Alien plants and their impact in the Mediterranean area

Chairs: Jordi López-Pujol, Olja Vasic

6.1 Carlos Gómez-Bellver - Botanical gardens as permeable systems for alien plants: Introduction, escape, and intra-garden dispersal dynamics—a case study of the Barcelona Botanical Garden.

6.2 Lina Podda - Conservation and restoration of Sardinian coastal habitats invaded by alien plant species

6.3 Salvatore Cambria - Malta and Sicily an incomparable dimension but a surprising similar alien plant diversity

6.4 Milica Rat - Towards a prioritisation framework for invasive alien plants in Serbia: From updated checklists to management planning

6.5 Ouafae Benkhnigue - Floristic and ecological study of alien flora of Morocco

6.6 Javier Martínez-Fuentes- New steps on the cataloging of alien flora in the Pyrenees

6.7 Salma Shaltout - Reassessment of the worst invasive alien plant species according to IUCN EICAT criteria in Egypt

6.8 Mine Koçyiğit - Melissopalynological insights into honey bee foraging on invasive alien plants in Türkiye

6.1

Botanical gardens as permeable systems for alien plants: Introduction, escape, and intra-garden dispersal dynamics—A case study of the Barcelona Botanical Garden

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The historical role of botanical gardens as sources of plant knowledge has always been highly significant. However, they have also inadvertently contributed to the introduction of alien species into surrounding areas. Today, botanical gardens not only make living plant collections accessible to the public, but also provide scientific information, promote public awareness of biodiversity, and generate, to a large extent, scientific publications based on their day-to-day experience.

The Barcelona Botanical Garden (JBB) is located in a privileged area on Montjuïc hill, in the southern part of the city of Barcelona and in close proximity to the sea. It hosts more than 2,000 species, with a strong representation of the characteristic flora of the world's main Mediterranean regions: the Mediterranean Basin—including Macaronesia (particularly the Canary Islands), California, Chile, South Africa, and southwestern Australia. Each species is grouped by ecological affinity into specific vegetation communities (phytoepisodes), including species ranging from structural elements to several threatened taxa.

The garden fence is composed of wooden logs spaced approximately 20 cm apart. This arrangement allows visual permeability but also facilitates the exchange of plant propagules across both sides. During the last two years, we have non-intensively recorded native and alien flora within and outside the garden boundaries. Four main dispersal dynamics can be identified: (i) native or (ii) non-native plants appearing (sub)spontaneously within the garden that have never been intentionally cultivated, (iii) non-native cultivated plants that escape beyond the garden boundaries, and (iv) other cultivated species appearing in phytoepisodes different from those where they were originally planted. Overall, we have recorded more than 110 spontaneously occurring native species and over 100 alien species, including taxa escaping from cultivation within the garden as well as others colonising the garden from surrounding areas outside their natural distribution, some of which exhibit a clearly invasive character.

Keywords: Alien plants, Botanical garden, Dispersal dynamics, Mediterranean flora, Native species.

6.2

Conservation and restoration of Sardinian coastal habitats invaded by alien plant species

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Coastal ecosystems are among the environments most severely affected by biological invasions, largely due to increasing anthropogenic pressures, particularly those associated with tourism. The impacts of these invasions are especially severe where they lead to local extinction of highly specialized and narrowly distributed native *taxa*. Sardinia is a continental island located in the central-western Mediterranean Basin, representing a meso-hotspot within the Tyrrhenian macro-hotspot and the wider Mediterranean mega-hotspot, one of the world's major biodiversity hotspots [1]. The island has the longest coastline among Italian regions, accounting for approximately one quarter of the national total. Although several relatively undisturbed coastal areas remain only marginally affected by Invasive Alien Species (IAS), many sites are currently experiencing extensive invasions by multiple *taxa* across dune, rocky shore, and wetland systems.

Over the last decades, Sardinian coastal environments have been the focus of various conservation projects involving direct actions to reduce the threat posed by IAS (e.g., LIFE projects PROVIDUNE, RES MARIS and SEEDFORCE, as well as projects funded under the Prioritized Action Framework and by the Sardinian Regional Government).

Here, we present a widely replicable approach from Sardinia that starts by assessing the occurrence and distribution of invasive plants in the most sensitive coastal habitats, followed by ecological studies of key taxa. In addition, our strategy aims to implement eradication and control measures in accordance with the objectives of the EU Nature Restoration Law (Regulation 2024/1991). Restoration activities include the collection, conservation and propagation of local germplasm from native species [2], thereby enhancing habitat recovery, increasing ecosystem resilience. Native plant use is fundamental for restoring ecological integrity while preserving the genetic diversity of natural populations.

Our approach integrates invasive species management with ecological restoration and *ex situ* conservation, providing a comprehensive framework that can be transferred to other Mediterranean coastal regions.

Keywords: Biodiversity, Eradication, Invasive plants, Mediterranean Basin, Seed bank.

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6.3

Malta and Sicily an incomparable dimension but a surprising similar alien plant diversity

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Within the framework of the RECLAIM project, funded by Interreg Italia–Malta, an updated database of the alien flora of Sicily and the Maltese Islands was developed. The study provides a comprehensive overview of non-native plant species across the two central Mediterranean insular systems, aiming to improve knowledge on their distribution patterns and ecological drivers. In addition, a detailed study was carried out on the distribution of each alien taxon in Sicily and Malta, highlighting its presence in the different areas of the islands, as well as assessing the altitudinal range, the invaded habitats, the risk of spread and establishment, and the possibility that the species may be introduced into either of the two territories where it is not yet present. Ellenberg indicator values were also calculated for each species to assess their ecological preferences in terms of light, moisture, soil reaction, and nutrients, thereby improving the understanding of the environmental conditions driving their distribution. The results indicate a similar number of alien plant species in both regions, despite the significant difference in surface area (25832 km2 versus 316 km2) associated however with smaller differences in terms of population (4 772 838 vs 563.443). This finding supports the tendency of alien species to concentrate in low-altitude environments, which can be explained both by the predominance of species originating from warm climates and by the higher levels of human disturbance in lowland areas, where urbanization and land-use intensity are greater. The habitats under the greatest pressure are coastal ones, such as dune systems (habitats 2110 and 2210), xerophilous grasslands (6220* and 5330), and scrub formations (5330, 9320), whereas overall synanthropic environments, such as roadsides, gardens, and agricultural areas, are the most species-rich in alien plants. The comparison between the two islands also highlights relevant biogeographical differences. Several invasive species recorded in Sicily have not yet become naturalized in Malta, while in other cases species native to Sicily are present and naturalized in Malta, despite not being native to the Maltese flora. The alien flora of Malta shows a significant imbalance, with casual species prevailing over naturalized ones when compared with Sicily, probably due to the presence of numerous species restricted to gardens and, more generally, to confined areas. These patterns reflect differences in introduction pathways, ecological conditions, and stages of invasion between the two island systems. Overall, the study emphasizes that an integrated and synergistic approach among those working in the field of conservation in Sicily and Malta is essential for effective monitoring and for preventing the further spread of invasive alien plant species in the central Mediterranean region.

Keywords: Mediterranean area, Plant invasions, Island ecosystems, Anthropogenic habitats.

6.4

Towards a prioritisation framework for invasive alien plants in Serbia: From updated checklists to management planning

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Research on invasive alien plants in Serbia has intensified over the last two decades, resulting in regional and national checklists, floristic surveys, and increased knowledge of species distribution. However, management approaches remain fragmented, and a comprehensive national framework for the prioritisation and control of invasive plant species is still lacking. Existing data reveal considerable differences among invasive taxa in their distribution patterns, ecological impacts, invasion dynamics, and management feasibility, indicating that uniform management approaches are insufficient. To address this issue, an updated synthesis and integrated prioritisation framework for invasive alien plants in Serbia is proposed, based on historical records and recent field investigations. Emphasis is placed on distinguishing between species requiring rapid eradication, those demanding long-term control in sensitive habitats, and widespread ruderal taxa for which eradication is unrealistic. This approach highlights the importance of habitat-specific and regionally differentiated strategies, especially considering Serbia's biogeographical diversity and heterogeneous landscape structure. Special attention is given to invasive plants recorded in protected and semi-natural habitats, including wetlands, riparian ecosystems, grasslands, and mountain regions. Recent findings, such as the occurrence of *Sigesbeckia orientalis* within the protected wetland area of Obedska bara, underscore the need for early detection and coordinated regional monitoring. In contrast, widespread ruderal species such as *Ambrosia artemisiifolia* and *Conyza canadensis* require management focused primarily on mitigation and monitoring. Some woody invasive species present additional challenges due to their ability to colonise both urban and natural habitats. *Ailanthus altissima* is notable for its spread across urban infrastructure, disturbed sites, riparian vegetation, and semi-natural forests, while *Amorpha fruticosa* poses a major threat to sensitive wetland ecosystems through dense population development and habitat transformation. The proposed framework aims to support future national management strategies by integrating floristic, ecological, and biogeographical criteria into invasive species assessment and prioritisation in Serbia.

Keywords: Invasive alien plants; Prioritisation framework; Management strategies; Serbia; Protected ecosystems

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6.5

Floristic and ecological study of alien flora of Morocco

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Morocco, situated in the southern Mediterranean Basin, represents a major biogeographical crossroads owing to its remarkable climatic, geological, and topographical diversity, which sustains an exceptionally rich flora. Nevertheless, knowledge of alien plant species within the country has remained largely fragmented, with no comprehensive nationwide synthesis previously available. This study fills this gap by providing the first comprehensive inventory and overall assessment of Morocco's alien vascular flora, drawing on field botanical surveys, a critical analysis of the floristic literature, and data from the most reliable major international floristic databases.

The results of our study enabled us to establish a preliminary list of 337 taxa, distributed across 205 genera and 62 families. The most speciose families include Asteraceae (45 taxa), Poaceae (35), Fabaceae (33), Amaranthaceae (30), and Solanaceae (30), while the genera Amaranthus L., Solanum L., and Euphorbia L. exhibited the highest species richness. The predominance of American (32.03%) and Asian (27.27%) origins reflects longstanding anthropogenic introduction pathways linked to historical trade networks. Therophytes constituted the dominant life form (50.41%), followed by phanerophytes (18.43%).

Naturalized species accounted for the largest share of alien flora (222 taxa; 65.88%), of which 66 were classified as invasive, 7 as emerging, and 4 as transformative, underscoring a considerable potential to disrupt ecosystem structure and functioning. Alien taxa were predominantly associated with ruderal and anthropogenically disturbed habitats.

To complement our study of alien flora introduced to Morocco, a second list was compiled focusing on cultivated taxa. After more than five years of fieldwork, we recorded over 1,300 cultivated taxa across Morocco, used for ornamental, agricultural, agri-food, agro-industrial, and medicinal purposes. These findings highlight the growing ecological significance of alien plants in Morocco and underscore the urgent need for targeted ecological assessments to inform evidence-based management and conservation strategies.

Keywords: Naturalized plants; Invasive species; Mediterranean region; North Africa; Morocco.

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6.6

New steps in the cataloging of alien flora in the Pyrenees

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Biological invasions are an increasing threat to biodiversity and ecosystems worldwide. Mountain ecosystems, traditionally considered more resistant to biological invasions, have become increasingly vulnerable due to human activities and climate change, which facilitate the spread of non-native plants to higher elevations. Improving our understanding of these invasions is therefore essential for their prevention and management. The Pyrenees constitute a particularly relevant case study due to their exceptional floristic richness, resulting from the wide diversity of climatic, topographic, geological, and ecological conditions across the mountain range. The *Atlas of the Flora of the Pyrenees* (https://atlasflorapyrenaea.eu/), developed through the cross-border projects FloraPyr Avance and FloraPyr 3D (funded by the INTERREG POCTEFA program), documents more than 3,600 native taxa confirmed in the Pyrenees since 1960. Within the framework of these projects, a revised, standardized, comprehensive, and up-to-date checklist of alien flora has also been compiled. To date, this checklist includes more than 700 taxa and will soon be expanded through the incorporation of records from the citizen science platform iNaturalist. In this contribution, in addition to presenting this checklist, we analyze the main ecological and biological characteristics of alien plants in the Pyrenees, and identify their principal spatial and temporal distribution patterns based on occurrence records and collection dates. Furthermore, we aim to develop a decision tree adapted to the Pyrenean dataset to assess the invasion status of each taxon, distinguishing between casual, naturalized, and invasive species. The results of this work will support the design and implementation of effective prevention, early detection, and management strategies aimed at limiting the introduction and spread of alien plant species across the Pyrenees. Ultimately, this will contribute to reducing their impacts on native species and ecosystems.

Keywords: Alien flora, Invasive alien species, Mountains, Pyrenees.

6.7

Reassessment of the worst invasive alien plant species according to IUCN EICAT criteria in Egypt

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Egypt is considered one of the oldest countries in the world whose people have been interested in agriculture throughout various civilizations until our modern age. Egypt is also the only country in the world that has remnants of plants of ancient cemeteries that was placed with mummies for use as food or for joy the other day. [1] Invasive species (both plants and animals, however our focus in the current study is the invasive plant species) pose a significant threat to biodiversity and ecosystems worldwide, and Egypt is no exception. [2] These species, often introduced through human activities including importing for ornamental purposes, can outcompete native flora, disrupt ecosystems [3,4], and cause economic damage [5]. As reported by Shaltout *et al.* (2020), alien plants in Egypt contribute about 11.7 % of the Egyptian flora. On the other hand, this study identifies seven of the most dangerous invasive alien plant species based on three key impact criteria: high water consumption, secretion of inhibitory compounds, and competitive replacement of native vegetation. These species (*Azolla filiculoides, Pontederia crassipes, Neltuma juliflora, Carpobrotus edulis, sesuvium portulacastrum, Ipomea carnea* and *Basia indica*) are further classified according to the IUCN categories of invasiveness. In addition to assessing their ecological threats, we propose sustainable reuse strategies that turn these species into environmental assets. [6] These include utilizing their high capacity for heavy metal absorption and water purification, as well as exploiting their strong dispersal ability and high protein content to produce natural fertilizers. This dual approach aims to mitigate the negative impacts of invasive species.

Keywords: Invasive, Plant, EICAT, Egypt, Biological Invasion

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6.8

Melissopalynological insights into honey bee foraging on invasive alien plants in Türkiye

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Invasive alien plant species represent one of the major threats to native biodiversity and ecosystem functioning. At the same time, many invasive plants produce abundant nectar and pollen resources that can attract pollinators, including honey bees (*Apis mellifera*). Understanding the interactions between honey bees and invasive plant species is therefore important for evaluating their ecological impacts and potential contribution to the spread of these plants [1].

This study aims to investigate the role of invasive plant species as foraging resources for honey bees in Türkiye using melissopalynological analysis. Honey samples collected from different regions of Türkiye were analyzed to identify pollen types and determine the presence of invasive alien plant species within the pollen spectra. Pollen grains were identified using standard melissopalynological techniques and reference pollen atlases.

Preliminary results indicate that several invasive plant species are frequently visited by honey bees and contribute to the pollen composition of honey. Species such as *Robinia pseudoacacia*, *Ailanthus altissima*, *Amorpha fruticosa*, and *Erigeron canadensis* were detected in multiple samples. These species are known for their high nectar production and long flowering periods, which make them attractive resources for pollinators [2].

The findings suggest that honey bees may play a role in the pollination and potential spread of invasive plant species in different habitats. Melissopalynology provides valuable indirect evidence of plant–pollinator interactions and can serve as an effective tool for monitoring invasive plants in the landscape [3]. This approach may contribute to a better understanding of invasion dynamics and help support management strategies aimed at protecting native flora and ecosystem integrity.

Keywords: Honey bee, Invasive alien plants, Melissopalynology, Pollen, Plant–pollinator interactions

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Symposium 7- New Natural Sources for Medicinal Usage: Marine Organisms, Fungi, Endophytes, etc.

Chairs: İlkay Erdoğan Orhan, Funda Nuray Yalçın

7.1 Vassilios Roussis- The red alga *Laurencia*: Where biodiversity meets chemodiversity

7.2 Leandros Skoultsounis - Indigoids: From natural dyeing agents to selective kinase inhibitors

7.3 Ilkay Erdogan Orhan - Promising potential of natural products from Turkish marine and fresh water ecosystem

7.4 Erdal Bedir - Fungal biotransformation: A route to novel and bioactive metabolites

7.5 Anna Beresova Guttova - Climate and substrate filtering in Mediterranean lichens: A case study from the genus *Solenopsora*

7.6 Efstathia Ioannou - New bioactive diterpenes from brown algae of the genus *Dictyota* from the Aegean and Ionian seas

7.7 Mustafa Ünver Kurt - Marine-derived *Streptomyces* sp. L8A39 from the İzmir Peninsula as a source of cytotoxic metabolites against drug-resistant A549 cell line

7.8 Zehra Torun - Hidden jewel in the Mediterranean: Anticancer potential of marine-associated fungus *Fusarium oxysporum e*xtract

7.1

The Red Alga *Laurencia*: Where biodiversity meets chemodiversity

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The cosmopolitan red algal genus *Laurencia* currently includes 146 taxonomically accepted species. Thorough anatomical studies have revealed that *Laurencia* is a highly diverse genus, encompassing species that display distinctive features, usually diagnostic at the generic level. In 1967 Saito was the first to divide *Laurencia* into two subgenera and the genus has thereafter been referred to as the "*Laurencia* complex". Successive detailed studies on the vegetative and reproductive structures of the included species and more recent investigations based on molecular sequences of the plastid-encoded gene rbcL have led to a further division of the "*Laurencia* complex", which now comprises the genera *Laurencia*, *Osmundea*, *Chondrophycus*, *Palisada*, *Yuzurua* and the genus *Laurenciella*, which is morphologically identical with the genus *Laurencia*, but differs in the rbcL sequence.
Laurencia is considered one of the most prolific genera and even though it has been investigated intensively over the last 60 years, many new molecules are being reported continuously. The observed extraordinary chemical variation of *Laurencia*, even within morphologically homogeneous species and populations, has been the subject of numerous studies that have provided frequently contradictory explanations.
This paradox intrigued us to investigate a large number of individually collected specimens from an isolated *Laurencia* population from the Greek coastlines. Every specimen was classified by classical systematics in parallel to molecular systematics criteria and was analysed by our chemical profiling fingerprinting platform. The results of this combinatorial study and the new isolated metabolites will be presented.

Keywords: *Laurencia*, Red algae, Secondary metabolites, Chemodiversity

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7.2

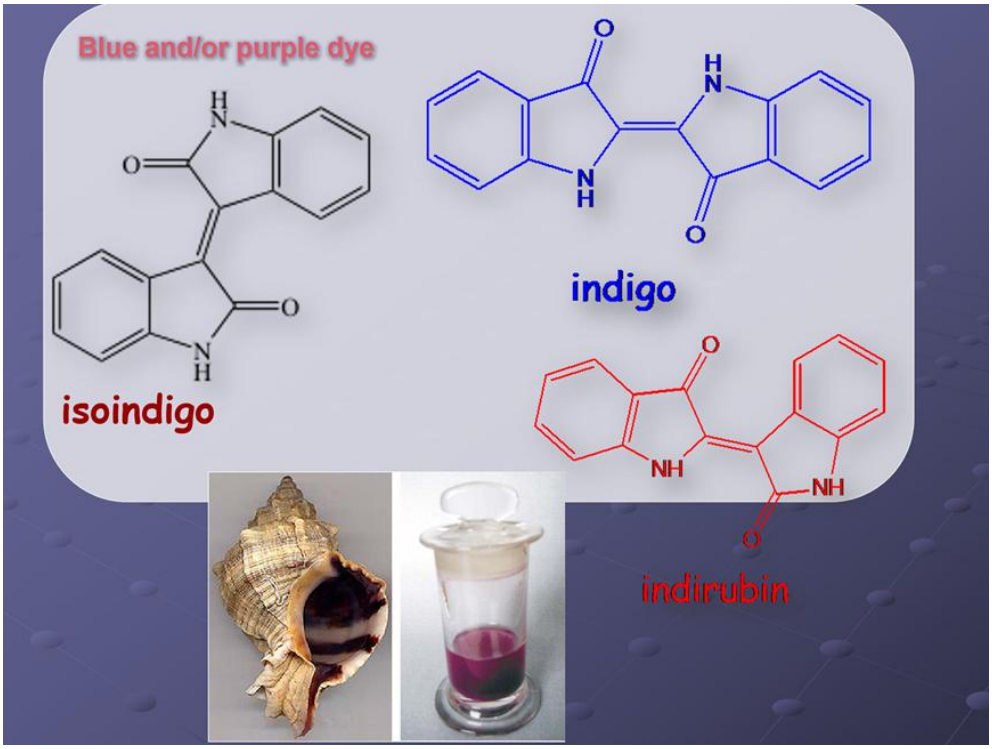
Indigoids: From natural dyeing agents to selective kinase inhibitors

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Indirubin, indigo and isoindigo are the core representatives of a rather small category of bisindole alkaloids referred to as indigoids which are the most used color throughout the Human history. These compounds are the colored constituents of the natural dyes Indigo and the famous molluscan Tyrian purple, used throughout the centuries for textile dying. In contrast with Indigo dyes, the major constituents of molluscan purple dyes are brominated indigoids. Nowadays, the use of natural dyes is very limited due to their replacement with cheaper synthetic dyes. Nevertheless, indigoids and especially indirubins have come to the timeliness due to the vast range of biological activities, which in many cases have their origin in traditional medicine. Chronic myelotic leukemia has been treated from the traditional Chinese medicine with the recipe Danggui Longhui Wan, a mixture of 11 herbal medicines. Eventually, the antileukemic activity was attributed to indirubin, which was detected in the mixture as a minor constituent. During the following years, indirubin and its halogenated analogues were found to possess a vast range of biological effects in stem cells, cardiac, renal, and pancreatic cells, even in parasitic organisms. In addition, brominated indirubins have been utilized as tools for the exploration of neurodegeneration and cancer. In most of the cases, all of the above effects can be associated with the interaction of indirubins with important molecular targets such as members of the family of protein kinases, placing them among the most promising nature-derived drug candidates.

Keywords: Indigoids, Kinase inhibitors



7.3

Promising potential of natural products from Turkish marine and fresh water ecosystems

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Aquatic and marine organisms, ranging from marine sponges and microalgae to freshwater and marine macroalgae, represent a prolific bioresource for discovering novel therapeutic agents. Marine natural products (MNPs) offer diverse chemical entities with unique mechanisms of action. Türkiye possesses an exceptional geographical advantage for marine and aquatic research, being a peninsula surrounded by four distinct bodies of water: the Mediterranean Sea, the Aegean Sea, the Sea of Marmara, and the Black Sea, which together create a vast coastline spanning more than 8,000 km. This unique transitional zone bridges different marine ecosystems, offering an immense and largely untapped bioresource of macroalgae, microalgae, sponges, and other aquatic organisms. Türkiye is uniquely bounded by four distinct seas—the microtidal, high-salinity Mediterranean and Aegean hosting rich biodiversity, the stratified, brackish Black Sea influenced by major river runoffs, and the Marmara Sea serving as a vital transitional biological corridor between them.

From our research perspective, exploring these diverse waters has continuously revealed valuable phytochemicals and active extracts with potent pharmacological activities—ranging from anticancer and antimycobacterial agents to enzyme inhibitors and sponge-derived terpenoids with broad-spectrum antiprotozoal and antileishmanial activities, as well as freshwater macroalgae showing significant antimycobacterial efficacy against *Mycobacterium tuberculosis* [1,2]. Furthermore, our screenings of marine macroalgae have identified species with remarkable enzyme inhibition, such as *Dictyota dichotoma* var. *intricata*, alongside high larvicidal and adulticidal properties against disease-vector mosquitoes like *Aedes aegypti* [3].

Given this rich marine and freshwater biodiversity, Türkiye holds a powerful position to drive significant advancements in marine biotechnology, drug discovery, and environmental sciences. Collectively, these findings underscore the vast pharmaceutical potential of aquatic biodiversity in providing advanced pharmacological leads and eco-friendly agents.

Keywords: Marine natural products, Marine pharmacognosy, Fauna, Biodiversity, Aquatic ecosystems

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7.4

Fungal biotransformation: A route to novel and bioactive metabolites

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Biotransformation, the use of living systems or their enzymes to chemically modify molecules, offers a powerful complement to synthetic chemistry, particularly for affording structurally complex compounds that are difficult or costly to prepare by conventional routes. Our team has focused on a specific variant of this approach: using plants' endophytic fungi to biotransform plant secondary metabolites, and then evaluating some of the resulting metabolites for cytoprotective activity and against cellular senescence. This interest is motivated by the growing societal burden of age-related diseases. Hallmarks of aging, such as loss of proteostasis, telomere attrition, and elevated ROS, drive disorders including cardiovascular disease, neurodegeneration, and cancer, creating sustained demand for new preventive and therapeutic agents. Natural products remain a rich source of candidates for cellular regeneration and healthy aging, owing to their structural diversity.

In this presentation, I will first describe our endophytic biotransformation studies of sapogenins and the resulting metabolite library. I will later focus on the effects of some of these metabolites on cellular senescence, with an emphasis on the NRF-2/proteasome/telomerase axis and neuroprotection. I will then highlight endophyte-mediated biotransformation as a productive strategy for expanding the chemical space around bioactive natural product scaffolds.

Keywords: Biotransformation; Endophytic fungi; Cellular aging; Natural products; Cytoprotection

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7.5

Climate and substrate filtering in Mediterranean Lichens: A case study from the genus *Solenopsora*

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The Mediterranean biome is characterized by strong environmental heterogeneity, long-term climatic stability, and a high diversity of rocky habitats that support specialized biota, including organisms adapted to chasmophytic niches. Among these, saxicolous lichens provide an underexplored opportunity for understanding how climatic gradients and substrate properties shape species distributions and symbiotic associations in environmentally constrained landscapes. Examination of distribution patterns in saxicolous species of the genus *Solenopsora* showed, that several taxa closely track the extent of the Mediterranean climatic domain. Despite their dispersal potential, predicted habitat suitability remains largely confined to this biome, with little indication of range expansion beyond its boundaries under future climate scenarios. To disentangle the relative roles of regional climate and substrate specialization in lichen symbioses, we investigated patterns of holobiont variation in the ultramafic-associated lichen *Solenopsora liparina* across its distribution range. Using *S. liparina* occurrence data and performing metabarcoding sequencing of its symbiotic partners at community level we observed variation in algal photobiont and associated fungal assemblages under contrasting environmental conditions. Our results suggest that persistence of lichens in ultramafic substrates relies on flexible symbiotic partnerships shaped mainly by climatic conditions. At a broader scale, the strong correspondence between *Solenopsora* distributions and Mediterranean climatic space highlights the potential of rock-dwelling lichen symbioses as indicators of biogeographic boundaries and environmental stability in heterogeneous landscapes.

Keywords: Holobiont, Metabarcoding, Ultramafites

Acknowledgment: The work was supported by the project VEGA 2/0046/25 and APVV-24-0473.

7.6

New bioactive diterpenes from brown algae of the genus *Dictyota* from the Aegean and Ionian seas

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The genus *Dictyota* (Dictyotaceae), comprising c. 40 species widely distributed in the tropical and subtropical regions of the Atlantic, Pacific and Indian Ocean, in the Sea of Japan, as well as in the Mediterranean Sea, is one of the most interesting genera of brown algae, with a rich chemical profile, characterized mainly by diterpenes and, to a lesser extent, sesquiterpenes.

Secondary metabolites isolated from species of the genus *Dictyota* demonstrate a wide spectrum of bioactivities, such as antibacterial, antifungal, antiviral, antifouling, cytotoxic and anti-inflammatory activity.

Over the last decades, we have collected from different localities in the Aegean and Ionian seas a high number of specimens belonging to the genus *Dictyota*, which have been submitted to analysis of their chemical profiles either through metabolomic analyses or through phytochemical analysis, leading so far to the identification of a high number of diterpenes, including several new natural products. Their isolation, structure elucidation and bioactivity evaluation will be presented.

Keywords: *Dictyota*, Brown algae, Secondary metabolites, Bioactivity

Acknowledgment: This project has received funding from the European Union Horizon Europe under the COMBO project (CL6-CircBio01-11, grant agreement No 101135438).

7.7

Marine-derived *Streptomyces* sp. L8A39 from the İzmir Peninsula as a source of cytotoxic metabolites against drug-Resistant A549 cell line

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Cancer remains a major global health challenge, with therapeutic resistance frequently compromising clinical outcomes. Although terrestrial actinomycetes have historically yielded approximately 40% of FDA-approved anticancer drugs derived from natural products, the clinical translation of microbial metabolites has remained limited since 1992, except for romidepsin. More recently, promising clinical studies of salinosporamide A, isolated from a marine actinomycete, have renewed interest in marine ecosystems as underexplored reservoirs of bioactive chemical scaffolds. Here, we investigated marine actinomycetes isolated from coastal sediments of the İzmir Peninsula in the Aegean Sea for cytotoxic metabolites against lung cancer.

A total of 945 actinomycete isolates were recovered from 46 sediment samples using four isolation media, and 25% of the crude extracts exhibited cytotoxicity against A549 lung adenocarcinoma cells in MTT assays. Based on their bioactivity and chemical profiles, five potent isolates were selected for metabolomic profiling, phylogenetic characterization, selectivity assessment, and synergy analyses with cisplatin in drug-resistant A549 cells. Taxonomic analysis confirmed that all five isolates belonged to the genus *Streptomyces*. Feature-based molecular networking and MS/MS-based dereplication tentatively annotated known secondary metabolites, including the reported anticancer agents staurosporine and actinomycin D, alongside several unannotated molecular clusters. All five extracts demonstrated selective cytotoxicity and synergistic interactions with cisplatin. Integration of these multilayered data identified that *Streptomyces* sp. L8A39, a novel isolate, is the most promising candidate for 40-liter fermentation. Bioactivity-guided fractionation of the resulting extract yielded new phenazine derivatives, together with staurosporine and related metabolites.

These findings highlight marine-derived *Streptomyces* strains from İzmir coastal ecosystems as an unexploited source of structurally diverse chemotypes with potential to overcome drug resistance in lung cancer. Elucidation of the primary mechanisms of action of the isolated metabolites is currently underway.

Keywords: Marine pharmacognosy, *Streptomyces*, Cytotoxicity, Metabolomics, Synergy

Acknowledgment: This study was supported by TÜBİTAK (PN: 122R077), and we are grateful to Prof. Dr. Ahmet Ceyhan Gören for providing access to the LC-MS/MS facility.

7.8

Hidden jewel in the Mediterranean: Anticancer potential of marine-associated fungus *Fusarium oxysporum* extract

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The World Health Organization (WHO) states that cancer is the leading cause of death globally, with high incidences of diagnosis and mortality. The primary cause of cancer is free radicals, which are produced by increased environmental factors and stressors leading to cellular pathogenesis. There is increasing interest in the use of natural products for the treatment and prevention of diseases. Organisms that live in saline and freshwater environments, such as oceans, seas, rivers, and lakes, produce novel active chemicals to survive extreme environmental conditions [1]. In this study, anticancer and radical scavenging activities of the methanol extract of the *Fusarium oxysporum* fungus isolated from the *Petrosia ficiformis* sponge in Samandağ Port (Hatay, Turkiye) was investigated. The fungal extract exhibited IC_{50} values of 254.3 µg/mL for the breast cancer cell line (MCF-7) and greater than 400 µg/mL for the murine fibroblast cell line (L929). In the DPPH• radical scavenging test, it exhibited moderate antioxidant activity with an IC_{50} value of 5.32 mg/mL. According to the National Cancer Institute (NCI) and the Geran Protocol [2], *F. oxysporum* exhibits as a viable source for new anticancer candidate compound investigations.

Keywords: Marine fungi, Cytotoxicity, Antioxidant, Endophytic fungus

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Acknowledgment: This study is supported by the Inonu University Scientific Research Projects project coded TOA-2025-4213.

Symposium 8- Biosystematics in the Mediterranean area (Young Scientist Symposium)

Chairs: Karol Marhold, Christoph Oberprieler, Lorenzo Peruzzi

8.1 Jacopo Franzoni - Advances in the systematics of wild carnations (*Dianthus*) in the central Mediterranean

8.2 Murat Erdem Güzel - On the Identity of *Crepis dioscoridis* (Asteraceae): Evidence from Greece and Türkiye

8.3 Osman Erol - Rapid speciation and centers of diversity: Case studies across the genus *Crocus* (Iridaceae) in Türkiye

8.4 Jose Luis Villar - Current status of *Tamarix* taxonomy in the Mediterranean region: Critical groups and future scopes

8.5 Pia Donhauser - Integrative species delimitation in the North-West African genus *Rhodanthemum* (Compositae, Anthemideae)

8.6 Batıkan Günal - An Assessment of the Taxonomic Complexity of the *Erigeron acris* Group in Türkiye

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8.8 Seher Güven - Palynological Characteristics of the Registered Tea (*Camellia sinensis*) Cultivars in Türkiye

8.1

Advances in the systematics of wild carnations (*Dianthus* L.) in the central Mediterranean

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The genus of wild carnations (*Dianthus* L.) is a species-rich group with a diversity hotspot in the Mediterranean Basin [1]. Nevertheless, the high rates of diversification in this region, combined with frequent polyploidization events and high phenotypic responsiveness to environmental variation, have resulted in taxa described in the Mediterranean that rarely represent well-supported species hypotheses. Such unreliable taxonomies hamper evidence-based conservation actions and prioritization [2], thus highlighting the urgent need for systematic and taxonomic studies. Here, we present the advances made in the systematic study of two species complexes (the *D. virgineus* and *D. balbisii* complexes), which have been investigated in recent years by means of integrative taxonomy. A general pattern of taxonomic inflation emerges in these two species complexes, where most morphology-based taxa do not represent evolutionarily distinct lineages or statistically differentiated morphological groups. The traditionally recognized 21 taxa in the *D. virgineus* complex belong to a single genetic lineage distributed throughout the central Mediterranean, consistently diploid ($2n = 2x = 30$), whose genetic and genome size variation follows geography rather than accepted taxonomy, and represent a morphometric *continuum* with 10 morphotypes. On the other hand, the taxa belonging to the *D. balbisii* complex are morphometrically and colorimetrically differentiated, except for those endemic to southern Calabria (southern Italy), despite homogeneous genome size variation. Although systematic research on wild carnations has advanced conspicuously in recent years, many species complexes in the Mediterranean and Europe still require attention. For instance, in Italy, out of the 56 accepted native taxa currently recorded, around 19 taxa, and related taxa or complexes, still await investigation from a systematic perspective. Filling this gap in knowledge would be vital for a taxonomic revision of the genus in order to provide a more reliable representation of Mediterranean and European biodiversity and providing a robust framework for conservation.

Keywords: Systematics, Taxonomy, Morphometry, Genetics, Cytogenetics

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8.2

On the Identity of *Crepis dioscoridis* (Asteraceae): Evidence from Greece and Türkiye

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Crepis dioscoridis L. is an annual or biennial herb distributed in the Western Mediterranean region. Although current literature treats the species as a single taxon, Babcock [1] recognized four subspecies. Literature data [2] and herbarium records indicate that the species is mainly distributed in Greece, while records from southwestern Türkiye (*D.* 41216!, *Tengwall* 670!, *Pichler* 424) require confirmation. Fieldwork in Türkiye, examinations of *C. dioscoridis* and the related *C. multiflora* in the herbaria KTUB and B, evaluations of images from the herbaria GAT and K, and DNA sequence analyses enabled assessment of the species and its distribution in Türkiye. Both *C. dioscoridis* and C. *multiflora* possess dimorphic achenes. However, *C. dioscoridis* has winged outer achenes, unlike *C. multiflora*. Inner achenes of *C. dioscoridis* show secondary ribs in addition to primary ribs, whereas *C. multiflora* has only primary ribs. At maturity, phyllaries in *C. dioscoridis* become rigid and tightly incurved, while in *C. multiflora* they remain less rigid and only slightly incurved. Molecular analyses also clearly separated the two species. Re-examination of the previous Turkish records showed that they (*Pichler* 424 not examined) do not belong to *C. dioscoridis*. These findings demonstrate that the two species are clearly separable by achene and capitulum features, and that *C. dioscoridis* does not occur in Türkiye. Greek specimens belonging to *C. dioscoridis* exhibit significant morphological variation as noted already by Babcock [2] and require further taxonomic evaluation.

Keywords: Achene morphology, *Crepis multiflora*, Molecular phylogeny, Taxonomy

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Acknowledgment: This study was supported by the Scientific and Technological Research Council of Türkiye (TÜBİTAK) under Grant No. 122Z966, which funded both fieldwork and laboratory analyses. Additional support was provided by the Office of Scientific Research Projects of Karadeniz Technical University (Grant No. 16885), which enabled a research visit of the first author to Freie Universität Berlin, Germany. I am grateful to Dr. Juraj Paule who is the curator of B for allowing me to study their rich *Crepis* collection. All underlying voucher specimens are deposited at the Botanic Garden and Botanical Museum Berlin (BGBM) and are available via the Global Genome Biodiversity Network (GGBN, Droege et al. 2014) and the Global Biodiversity Information Facility (GBIF).

8.3

Rapid speciation and centers of diversity: Case studies across the Genus *Crocus* (Iridaceae) in Türkiye

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Türkiye is a recognized center of *Crocus* diversity, due in large part to rapid ongoing speciation, which results in many endemics and species complexes with blurred taxon boundaries. The genus thus provides numerous case studies that allow us to follow speciation in real time and track centers of origin. Our work on crocuses highlights many facets of these concepts, covering anatomy and morphology, cytology and molecular work, showing how natural variation and its interplay with ecology creates constantly evolving taxonomic complexity that necessitates an integrated approach to avoid contradictory results. For instance, many closely related members of the *C. pallasii* complex (*Crocus* series *Crocus)*, have the same chromosome numbers but otherwise exhibit incredible diversity across their ranges and prove to be interesting case studies in discussions of ploidy. Meanwhile, series *Speciosi* shows remarkable genome size diversity even within populations. The genetic diversity of the *Crocus chrysanthus* (series *Biflori*) complex (currently all synonyms of *C. chrysanthus* s.l.) in Türkiye alone is so staggering that some would be better placed within an as-yet undefined series. Even some narrow endemics of Türkiye may show enough morpho-anatomical and molecular variety that they have proven to harbour more than one species, as in *C. gargaricus* (series *Reticulati)* and *C. mathewii* (series *Crocus*). While each taxon presents one fascinating example of the ongoing diversification of a genus, when taken as a whole, they tell a much larger story about speciation explosion and the formation of centers of diversity.

Keywords: Crocus, Iridaceae, Biodiversity

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8.4

Current status of *Tamarix* taxonomy in the Mediterranean region: Critical groups and future scopes

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Tamarix L. was recognised as a genus with a complicated taxonomy since the mid-19th Century [1]. With the last comprehensive monograph [2] dating from 1978, many uncertainties remain unsolved and a wide range in the number of accepted species can still be found, depending on the bibliographic sources [2, 3]. For the Mediterranean countries, the Euro+Med Plantbase accepts up to 26 species. Among those, only 13 are here considered to be undoubtfully native from the Mediterranean countries: *T. africana, T. aphylla, T. boveana, T. dalmatica, T. duelenzii, T. gallica, T. hampeana, T. minoa, T. nilotica, T. octandra, T. parviflora, T. smyrnensis* and *T. tetragyna.* The 13 species remaining can be classified as cultivated (*T. ramosissima* and *T. chinensis*) or belonging to species complexes that are in need of detailed studies to elucidate their definitive acceptance. For instance, the group of amplexicaul leaves and flowers with 10 stamens, including *T. passerinoides, T. macrocarpa* and *T. amplexicaulis* would need deep revision in order to achieve an actualised taxonomic organisation. Similarly, all the taxa morphologically related to *T. nilotica* need to be evaluated, those including *T. arborea, T. jordanis,* and *T. palaestina.* Species like *T. canariensis* and *T. mascatensis* should be discarded from the study area. The two remaining species (*T. kotschyi* and *T. gracilis*) are in need of re-evaluation, since their original range areas are extra-Mediterranean.

Factors such as the plasticity of morphological characters within species along the year or the phylogenetic proximity of clearly distinct species make taxonomic arrangements difficult. The achievement of proper taxonomic solutions for *Tamarix* can only be done by a combination of detailed morphological work, molecular phylogenetics and recognition of the plants in the field. But none of those tools used individually will produce definitive results.

Keywords: *Tamarix*, taxonomy, Mediterranean

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8.5

Integrative species delimitation in the North-west African genus *Rhodanthemum* (Compositae, Anthemideae)

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The genus *Rhodanthemum* B.H.Wilcox & al. (Compositae, Anthemideae) presently comprises 17 species distributed in NW Africa (mainly Morocco) and S Spain. Owing to the formation of hybrids whenever representatives of the genus share the same habitat, this syngameon is a focal study group in the CARRARA project, which aims at the establishment of objective methods of integrative species-delimitation in intensively hybridising genera based on herbarium specimens. We have used 92 accessions of *Rhodanthemum* and three of its sister-genera *Chlamydophora, Chrysanthoglossum,* and *Leucanthemum* to infer phylogenetic relationships among all described species of the former genus based on a SNP matrix gained by AFLPseq fingerprinting. Based on a total of 43,538 SNPs, a well-supported backbone phylogeny of *Rhodanthemum* emerged that was used subsequently to further elucidate the species delimitation of different groups of *Rhodanthemum* taxa. One such example of hybridization within the genus *Rhodanthemum* is the complex group comprising *Rh. gayanum* and *Rh. depressum*. *Rhodanthemum gayanum* is distributed throughout Morocco with several subspecies that can be clearly subdivided into genetic clusters that parallel their geographic distribution. Particularly in Morocco's High Atlas Mountains, where *Rh. depressum* also occurs, several intermediate samples can be found alongside the respective typical lineages, bridging the gap between *Rh. gayanum* and *Rh. depressum*. Between *Rh. depressum* and *Rh. gayanum,* there is a continuous elevational transition, with *Rh. depressum* occurring at high elevations, *Rh. gayanum* at low elevations, and intermediate samples between these two. The observed pattern of intermediate forms between the two taxa is also evident in morphological and ecological analyses based on eco-climatological and edaphic (soil-grid) variables. The combination of all three disciplines may contribute to an integrative taxonomy for this group of taxa. Other groups of taxa have also been studied using the same approach to resolve their taxonomic status and will be reported on in the present contribution.

Keywords: Integrative species delimitation, Genealogy, Morphology, Ecology, Geography

8.6

An assessment of the taxonomic complexity of the *Erigeron acris* group in Türkiye

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Asteraceae is one of the largest and most diverse angiosperm families, comprising approximately 25,000–35,000 species and exhibiting remarkable morphological and ecological variation [1]. Within the tribe Astereae, the genus *Erigeron* includes several taxonomically challenging groups in which diagnostic characters overlap and taxa have been treated inconsistently at the species or infraspecific level. Recent regional revisions have shown that material broadly identified as *Erigeron acris* may conceal substantially underestimated diversity [2]. As part of a doctoral taxonomic revision of *Erigeron* in Türkiye, Turkish representatives of the *E. acris* group were evaluated using field collections, specimens from national and international herbaria, relevant type material, and detailed morphological and morphometric analyses [3]. In accordance with previous taxonomic treatments, *E. pycnotrichus* was accepted at the species rank. Examination of the original material clarified the application of this name, and *Kotschy* 303 from the Bolkar Mountains was selected as the lectotype, allowing morphologically heterogeneous material previously associated with the name to be excluded from its type concept. Following the separation of *E. pycnotrichus*, the remaining Turkish specimens traditionally identified as *E. acris* were treated as *E. acris* sensu lato. Four recurring and morphologically distinguishable groups were recognized, tentatively corresponding to *E. acris*, *E. podolicus*, *E. orientalis*, and *E. serotinus*. These groups differed in combinations of vegetative and reproductive characters observed in both field and herbarium material. However, broader population-level sampling, detailed morphometric comparisons, direct examination of relevant type specimens, and evaluation of character stability across geographical and ecological gradients are still required to define their diagnostic boundaries more precisely. Overall, the Turkish *E. acris* group represents a morphologically heterogeneous and taxonomically complex assemblage. These findings highlight Türkiye as an important region for reassessing diversity within the group and provide a morphological framework for future taxonomic studies.

Keywords: *Erigeron acris* group, Species delimitation, Taxonomic complexity

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8.7

Revisiting *Campanula* (Campanulaceae) in Türkiye: Integrative taxonomy and insights into diversity, endemism, and phylogenetic complexity

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The Mediterranean Basin is widely regarded as a key biodiversity hotspot, defined by remarkable species richness, high levels of endemism, and rapid rates of diversification [1-3]. Campanulaceae Juss. highlights the taxonomic and evolutionary complexity of the Mediterranean flora, encompassing roughly 2400 species that display significant morphological variation across diverse ecological niches [4-5]. Within this family, the subfamily Campanuloideae Burnett comprises over 1000 species, mostly concentrated across temperate Eurasia and the Mediterranean area [4-5], where a large proportion of narrowly distributed endemic taxa are restricted to islands or isolated continental areas [6-7]. Despite this documented diversity, systematic relationships across many Mediterranean clades remain unresolved, and true diversity is likely underestimated in cases where morphological differences are subtle.

Campanula L., representing the largest genus within Campanulaceae Juss., includes approximately 455 species globally. Its geographical distribution spans primarily the temperate and subtropical zones of the Northern Hemisphere, extending into South Asia and Northern Mexico [4, 5, 8-10]. Because over 80% of the roughly 278 *Campanula* species recorded in the Mediterranean region are endemic, this zone is recognized as a primary center of diversification for the genus [11]. Among the temperate countries of the Mediterranean basin, Türkiye harbors one of the richest assemblages of *Campanula*. The genus is represented in Türkiye by nearly 150 taxa, with more than half of them being endemic [12-24].

Historically, the taxonomy of *Campanula* relied on morphological and karyological features; however, substantial morphological plasticity impeded reliable taxonomic delimitation [25-26]. Subsequent molecular phylogenetic studies demonstrated that traditional circumscriptions of *Campanula* are non-monophyletic, instead consisting of two major lineages and around 17 primary clades that together comprise roughly 600 species [27-29]. Even so, evolutionary relationships among taxa—particularly those originating from Mediterranean biodiversity hotspots—remain incompletely clarified [1, 29]. The evolutionary trajectory of *Campanula* has been heavily shaped by processes such as hybridization, polyploidy, and incomplete lineage sorting, while the geological history of the Mediterranean, notably the Messinian Salinity Crisis, played a pivotal role in driving patterns of speciation and diversification [7, 30-32].

In the present study, an integrative taxonomic framework combining detailed morphological evaluations with molecular phylogenetic data is applied to the Turkish representatives of *Campanula*. Extensive field sampling, herbarium reviews, and DNA sequencing analyses yield novel insights into species boundaries, sectional classification, and the broader phylogenetic structure of the genus. The findings

highlight Anatolia as a crucial diversification center for *Campanula* and underscore the vital role of integrative methods in resolving persistent taxonomic challenges within the group.

Keywords: Anatolia, *Campanula*, Campanulaceae, Taxonomy, Türkiye

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8.8

Palynological characteristics of the registered tea (*Camellia sinensis*) cultivars in Türkiye

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Tea (*Camellia sinensis* (L.) Kuntze) is one of the world's most widely consumed beverages and represents an economically and culturally important crop. However accurate characterization of tea cultivars remains a significant unresolved issue in terms of the conservation of local genetic resources, variety identification, and breeding programs. In the present study, the palynological characteristics of six registered tea cultivars (Zihni Derin, Ali Rıza Erten, Çaykur 1, Çaykur 2, Çaykur 3, and Çaykur 4) from Türkiye were examined using light microscopy and scanning electron microscopy. Palynological analyses were performed on pollen grains isolated by the acetolysis method from flowers of six registered tea cultivars grown under identical environmental conditions in the National Tea Gene Pool at the Atatürk Tea and Garden Cultures Research Institute (Rize, Türkiye). All cultivars exhibited tricolporate, isopolar, radially symmetrical pollen grains with a triangular outline in polar view, predominantly oblate in shape (Polar axis (P) / Equatorial axis (E) = 0.82–0.95), and a perforate-verrucate exine ornamentation. Although all cultivars shared a common pollen morphology, notable differences were observed among the examined cultivars in several quantitative palynological characters, including pollen size (polar and equatorial axes and P/E ratio), aperture characteristics (colpus and pore dimensions), and exine thickness. These findings showed that quantitative palynological characters provide reliable taxonomic markers for the characterization and identification of registered Turkish tea cultivars and constitute a valuable resource for germplasm conservation and future tea breeding studies.

Keywords: *Camellia sinensis*, Cultivar, Pollen morphology, SEM.

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Symposium 9- Beyond preservation: The evolving functions of Mediterranean herbaria

Chair: Adil Güner

9.1 Erich Helmut Freitag - The genus *Ephedra* (Ephedraceae, Gnetales) in Tunisia

9.2 Igor Boršić - The Herbarium collection of the Croatian Natural History Museum – CNHM as a source of data on the vascular flora of Mediterranean Croatia

9.3 Alessio Papini - The massive data production by scanning of the main Italian herbaria

9.4 Salvatore Tomasello - Museomics and type material disentangle long-debated species delimitation in the taxonomically complex *Xanthium* subsect. *Campylorrhyncha*

9.1

The genus *Ephedra* (Ephedraceae, Gnetales) in Tunisia

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We carried out a revision of the genus *Ephedra* (Ephedraceae) in Tunisia, including taxonomic, nomenclatural, and conservation updates. The study is based on the morphological examination of both living material from almost all over the country and herbarium specimens. A large portion of the herbarium specimens was collected by the second author. Numerous specimens from other herbaria were also consulted, either by visiting them, by requesting loans or through online resources. We were fully aware that identification of *Ephedra* samples by classical morphological characters is usually hampered by the fact, that the material does not contain male or female organs and that the vegetative branches of the different species only show few distinguishing characters which might be somewhat variable and/or overlapping. However, that can be compensated by experience and by observations in the field. The most important morphological characters used in our study were: Habit, diameter of green twigs, surface of twigs, color and structure of pith, size and structure of leaves, details of male and female cones, shape of pollen grains.
From the eight N African species, four are represented in Tunisia: *Ephedra altissima* with the varieties *altissima* and *wettsteinii*, *E. alenda, E. fragilis* with the varieties *fragilis* and *aurea,* and *E. nebrodensis*. *E. alenda* was so far usually considered as a subspecies of *E. alata* but morphological arguments and geographical separation are in favor of species rank as was suggested already by [1]. *E. fragilis* subsp. *fragilis* var. *aurea* is recombined here from the recently described *E. aurea* [2] which was found by us also in Tunisia. Further studies might show that *E. alata* and *E. procera* also occur in Tunisia. Conservation concerns are highlighted, particularly for *E. fragilis* var. *aurea* threatened by habitat destruction, and for the extremely rare *E. nebrodensis*.

Key words: Gymnosperms, N Africa, up- and downgrading of species

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9.2

The herbarium collection of the Croatian Natural History Museum – CNHM as a Source of data on the vascular flora of mediterranean Croatia

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The Herbarium Collection of the Croatian Natural History Museum – CNHM is one of 13 officially registered herbarium collections in Croatia [1]. Established in 1987, the Herbarium currently contains around 100,000 specimens of vascular plants and continues to grow. It contains three herbaria, namely the Herbarium of Higher Plants (Vascular Flora), the Trinajstić Herbarium, and the Algae Collection. The Herbarium of Higher Plants contains approximately 22,000 curated specimens of vascular plants, most of which were collected during field research in Croatia from its foundation to the present day. It also includes older herbarium sheets collected before its establishment, including specimens collected by Professor Ivo Pevalek, and four (of a total of nine) volumes of the *Gramina Hungarica* collection, edited and curated by Arpad Degen. The Trinajstić Herbarium was purchased in 2004 from Prof. Ivo Trinajstić (1933-2024). It contains about 60 000 herbarium sheets collected by Prof. Trinajstić in Europe, Asia Minor and parts of North America. Approximately 5,000 herbarium sheets, comprising nearly 14,000 specimens, have been curated.

In this work we conducted analyses of the data on the vascular flora in the Herbarium Collection of the Croatian Natural History Museum from the Mediterranean biogeographical region in Croatia, obtained from the Flora Croatica Database [2]. The results showed that the most numerous families by inventory numbers and herbarium specimens are Fabaceae and Poaceae, followed by Euphorbiaceae, Asteraceae and Brassicaceae. The highest collecting intensity occurred in the 1950s, 1960s and 1970s (for the Trinajstić Herbarium) and in the first decades of the 20th century (for the Herbarium of Higher Plants). The largest number of specimens was collected by Ivo Trinajstić, followed by Museum Adviser Suzana Buzjak (alone or with collaborators).

Keywords: Herbarium sheet, Herbarium specimen, Inventory number, Ivo Trinajstić, Mediterranean biogeographical region

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9.3

The massive data production by scanning of the main Italian herbaria

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In the context of the project CN5 (PNRR) and National Biodiversity Future Center (NBFC), we performed a massive scanning at high resolution of a large parte of the herbarium specimens conserved in Italy. To reach this goal, the activity established a partnership with the Dutch company Picturae, owner of equipment specifically designed to this goal, with an average weekly production of 60000 images of herbarium specimens.
After the first phase in Florence, centered on the HCI, other italian herbaria participated to the effort of digitization arriving at 4,250,000 specimens, most of them of the Mediterranean region. Together with the associated metadata, this initiative will make it possible to make available millions of samples for investigation at a distance. The digitization of a large number of herbarium specimen will produce a large databases of high resolution images, and is a relevant source of big data that are and will be always more used for the investigation of biodiversity [1]. The images (jpg format) are being transferred to a CINECA repository for testing methods of articial intelligence for investigation of high numbers of samples, using both the plant material and the metadata obtained from the label. The images will be available on GBIF and by the single herbaria websites.

Keywords: Herbaria, Digitization, Metadata, Artificial intelligence

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9.4

Museomics and the inclusion of types disentangling long-standing taxonomic controversies in *Xanthium* subsect. *Campylorrhyncha*

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Taxonomically Complex Groups (TCGs) are taxa difficult to delimit using standard classification, due to the presence of extensive morphological plasticity and phenomena such us uniparental reproduction, hybridization, and polyploidy [1]. With this study we aimed at testing modern integrative taxonomy methodologies and museomics to delimit (and discern between) species and subtle infraspecific diversity in the taxonomically complex genus *Xanthium* (Asteraceae). For the scope, we integrated coalescent based species delimitation and population genetics approaches, along with morphometric and niche modeling. The classification of *Xanthium* has been debated for centuries, with several described taxa, nowadays often lumped into a few, morphologically extremely variable and wide-distributed species [2]. We analysed over 140 herbarium specimens from *Xanthium* subsect. *Campylorrhyncha*, including over 30 type specimens, the oldest of which from the middle of the 18th century. We applied ancient DNA (aDNA) extraction techniques, target enrichment of over 1000 nuclear regions and sequencing of plastidial genomes, morphometrics of the infructescences (burs) and ecological analyses of bioclimatic and soil variables. Although results from the morphometric analyses did not prove to be very informative, DNA-based species delimitation and structure analyses, along with model selection via Marginal Likelihood, integrated with ecological data consented us to identify four specific entities. Further fine-scale analyses of within species genetic structure and morphometrics allowed us to propose a robust classification of the subtle diversity observed in some of the species. This study shows how type-inclusive museomics and integrative taxonomy can resolve long-standing systematic controversies and provide a solid basis for species identification and future research into TCG.

Keywords: Coalescent Model; Integrative taxonomy; Phylogenomics; Species delimitation; Subspecies.

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Symposium 10- Recent advances in Lamiaceae science

Chairs: Tuncay Dirmenci, Chunlei Xiang, Bryan Drew

10.1 Chunlei Xiang - Taxonomy, phylogenomics, biogeography and evolution of *Phlomoides* (Lamiaceae, Lamioideae)

10.2 Selami Selvi - From past to present: Ethnobotanical uses of Lamiaceae species in the Mediterranean region

10.3 Hye-Kyoung Moon - Repeated gynodioecy: A Window into reproductive evolution in Lamiaceae

10.4 Fei Zhao - Plastome and multi-locus phylogeny of *Ajuga* (Lamiaceae): Reassessing infrageneric classification

10.5 Bryan Drew - History of Lamiaceae in the Mediterranean region

10.6 Miguel Campos - Incomplete lineage sorting and pulsed introgression drive extensive cytonuclear discordance in the rapidly radiating *Sideritis* sect. *Empedoclia* (Lamiaceae)

10.7 Taner Özcan - *Anatolia*: Resolving a long-standing taxonomic puzzle in Menthinae

10.1

Taxonomy, phylogenomics, biogeography and evolution of *Phlomoides* (Lamiaceae, Lamioideae)

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Phlomoides Moench is the second largest genus in Lamioideae, comprising approximately 180 species distributed mainly in the Mediterranean region, Central Asia, the Himalayas, and the Hengduan Mountains. Despite its recent recircumscription, its generic limits, infrageneric classification, and evolutionary history remain poorly understood. Here, we reconstructed the phylogeny of *Phlomoides* using complete plastome sequences together with nuclear ITS and ETS data, sampling 132 species and eight varieties. Phylogenetic and morphological evidence supports the inclusion of eight traditionally recognized genera within *Phlomoides*, with *Metastachydium* and *Pseudomarrubium* reduced to synonymy [1]. All previous infrageneric classifications are shown to be inconsistent with phylogeny, and six well-supported clades are recognized, each characterized by potential morphological synapomorphies. Divergence time estimation and historical biogeographic analyses suggest that *Phlomoides* originated in the Hengduan Mountains or Central Asia during the Middle Miocene and subsequently diversified across Eurasia. Ecological niche analyses indicate that climatic differentiation, particularly in precipitation and temperature seasonality, has played a major role in lineage diversification. Several morphological characters, including pinnatipartite leaves, tuberous roots, and trichomes on the mericarp apex, appear to represent adaptations to drought [2]. A comprehensive taxonomic revision of Chinese *Phlomoides*, based on extensive field investigations and examination of more than 11,700 herbarium specimens, resulted in the recognition of four new species, four new records for China, and four new combinations. This study provides the first comprehensive phylogenomic, taxonomic, and biogeographic framework for Phlomoides and offers new insights into the diversification of one of the largest genera in Lamioideae.

Keywords: Chloroplast genome, Drought adaptation, Eremostachys, Molecular phylogenetics, Phlomideae

References:

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10.2

From past to present: Ethnobotanical uses of Lamiaceae species in the Mediterranean region

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Lamiaceae (Labiatae), commonly known as the mint family, is one of the largest and most diverse families of flowering plants, comprising approximately 236 genera and more than 7,000 species worldwide [1]. The Mediterranean Basin, characterized by remarkable floristic diversity, high levels of endemism, and a plant-use tradition spanning millennia, represents one of the world's major centers of ethnobotanical knowledge. Within this rich cultural heritage, Lamiaceae occupies a particularly prominent position owing to its diverse traditional uses, especially in medicine, food, and cosmetics. Its history of use, extending from the Neolithic period to the present day, reflects the enduring importance of genera such as *Origanum, Salvia, Thymus, Teucrium, Ajuga, Ziziphora, Mentha,* and *Sideritis* in the daily lives of Mediterranean communities. More than 600 Lamiaceae taxa belonging to 42 genera are known to be traditionally utilized throughout the Mediterranean region. Among the most widely used genera are *Salvia, Mentha, Thymus, Origanum,* and *Lavandula*, while *Salvia rosmarinus, Salvia officinalis, Origanum vulgare, Thymus vulgaris,* and *Mentha pulegium* are among the most prominent species. Medicinal uses are mainly associated with digestive and respiratory disorders, common colds, pain, infections, and various microbial conditions, whereas food-related uses predominantly include herbs, spices, flavoring agents, herbal teas, and other beverages [1,2]. Leaves, flowers, and aerial parts are the most frequently used plant materials, with infusion and decoction being the principal preparation methods. Essential oils and other secondary metabolites play a key role in the ethnobotanical significance of the family. α-Pinene, β-pinene, 1,8-cineole, menthol, limonene, and γ-terpinene are common constituents of the essential oils; thymol and carvacrol are particularly characteristic of *Thymus, Origanum, Satureja,* and *Thymbra*, whereas pulegone is prominent in *Mentha* and *Ziziphora*. Rosmarinic acid, caffeic acid, flavonoids, iridoid glycosides, and tannins further contribute to the biological and functional value of the family [2]. This rich body of traditional knowledge establishes Lamiaceae as a key component of Mediterranean biocultural heritage and an important resource for phytotherapy, pharmacognosy, functional foods, and natural-product research.

Keywords: Lamiaceae, Mediterranean, Ethnobotany, Traditional uses, Medicinal plants

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10.3

Repeated gynodioecy: A Window into reproductive evolution in Lamiaceae

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Among the diverse reproductive systems in Lamiaceae, gynodioecy has evolved repeatedly across multiple lineages. This recurring pattern raises a simple but important question: what can repeated gynodioecy tell us about reproductive evolution?

In this talk, I explore this question by integrating evidence from comparative morphology, reproductive biology, systematics, and phylogeny. Rather than treating gynodioecy as an isolated breeding system, I use it as a comparative framework for examining how reproductive diversity has evolved within Lamiaceae.

Drawing on examples from across the family, I discuss how repeated origins of gynodioecy provide insight into the evolution of reproductive systems and into the relationship between floral morphology and reproductive function. I also consider how studies of Lamiaceae can contribute to a broader understanding of reproductive evolution in flowering plants and highlight questions that remain to be explored.

By viewing repeated gynodioecy as a comparative evolutionary phenomenon rather than an isolated breeding system, this talk aims to provide a broader perspective on the origins and diversification of reproductive systems in flowering plants.

Keywords: Gynodioecy, Lamiaceae, Reproductive evolution, Breeding systems

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10.4

Plastome and multi-locus phylogeny of *Ajuga* (Lamiaceae): Reassessing infrageneric classification

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The genus *Ajuga* L. (Lamiaceae, Ajugoideae) comprises approximately 69 species distributed across Eurasia, Africa, and Australasia. Despite its ecological and economic importance, infrageneric classification and phylogenetic relationships within *Ajuga* have remained poorly resolved. Here, we establish a comprehensive phylogenetic framework for the genus by integrating plastome-scale data with extensive multi-locus nuclear and plastid sampling across its global distribution. Comparative analyses of complete plastomes from 21 accessions representing 19 species, including 12 newly sequenced, revealed a highly conserved quadripartite structure. Plastomes ranged from 149,963 to 150,740 bp, with a GC content of 38.2%–38.3%, and consistently encoded 133 genes. In addition, 781 simple sequence repeats, 832 long repeats, and 12 highly variable loci were identified. Broad-scale phylogenetic analyses based on seven plastid markers (*matK*, *ndhF*, *psbA-trnH*, *rbcL*, *rpl32-trnL*, *rps16* intron, and *trnL-trnF*) and two nuclear ribosomal regions (ITS and ETS) included 51 species representing all previously recognized infrageneric groups. Maximum likelihood and Bayesian inference analyses strongly supported the monophyly of *Ajuga*. Despite minor incongruences between

nuclear and plastid datasets, plastome and multi-locus analyses consistently recovered two well-supported major clades. This deep phylogenetic split corresponds closely to geographical distribution, separating a lineage extending from the Mediterranean to Central Asia from one predominantly distributed in East Asia. The two lineages are further supported by morphological characters, particularly upper corolla-lip shape, flower number per verticillaster, and corolla color. Our results demonstrate that traditional infrageneric classifications do not adequately reflect the evolutionary history of *Ajuga*, emphasizing the need for formal taxonomic revision. The genomic resources and phylogenetic framework presented here provide a foundation for future studies of species delimitation, diversification, and evolution in *Ajuga*.

Keywords: *Ajuga*, Ajugoideae, Plastome Evolution, Phylogenomics, DNA barcoding

10.5

History of Lamiaceae in the Mediterranean region

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Currently, the Mediterranean region is one of seven global hotspots of Lamiaceae (mint family) diversity. Despite the current ubiquity of the Lamiaceae throughout the region, however, the family has extensively colonized the Mediterranean region relatively recently. Here, I discuss the spatial and temporal history of the mint family and explore when and why the group expanded and diversified within the Mediterranean region.

Keywords: Mediterranean, Lamiaceae, Biogeography

10.6

Incomplete lineage sorting and pulsed introgression drive extensive cytonuclear discordance in the rapidly radiating *Sideritis* sect. *Empedoclia* (Lamiaceae)

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Incomplete lineage sorting (ILS) and introgressive hybridization generate cytonuclear discordance during plant speciation, yet disentangling their relative contributions remains challenging in rapidly radiating lineages where short internodes preclude complete lineage sorting. *Sideritis* sect. *Empedoclia* (Lamiaceae), a taxonomically complex Mediterranean group, represents an ideal system for addressing these questions. We reconstructed the evolutionary history of 59 accessions (50 ingroup taxa; 42 species and eight subspecies) using target-recovery of hundreds of single-copy nuclear orthologs and complete plastome sequences. Concatenated maximum likelihood and multispecies coalescent analyses recovered a rapid, star-like radiation with low quartet concordance (Q1 ≈ 0.51) and gene concordance factors (gCF ≈ 22%). Divergence time estimation placed the crown age at 5.32 Ma, with the entire diversification compressed within 5.32-1.82 Ma. Nuclear-plastome discordance was extensive (gRF = 0.83-0.88) but non-random (Procrustean cophylogenetic and gene-cloud analyses), and network analyses revealed a reticulate backbone (delta score = 0.418; h = 31 reticulations) rather than a single hybrid origin. Phytop, QuIBL, and Dsuite analyses showed that ILS is the largest identifiable contributor (mean ≈ 48%), while introgression is geographically restricted and pulse-like, with *S. hololeuca* as a recurrent recipient of gene flow. Integrating morphometrics, Mantel tests, Procrustes rotation, and phylogenetic signal metrics (Blomberg's K, Fritz's D, Pagel's λ) revealed extensive morphological homoplasy: most diagnostic characters lack phylogenetic signal, and all subspecific complexes were polyphyletic except *S. erythrantha*. Sect. *Empedoclia* is thus a classic rapid radiation in which morphology has converged across distantly related lineages, highlighting the need for integrative taxonomic revision.

Keywords: *Mediterranean Basin, Rapid radiation, Stachydeae, Homoplasy, Hybridization*

10.7

Anatolia: Resolving a long-standing taxonomic puzzle in Menthinae

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Micromeria cymuligera is a rare and very local endemic endemic species of Türkiye, and its taxonomic and phylogenetic affinities have remained unclear since its description in 1879. The rediscovery of the species in 2011 provided an opportunity to reassess its systematic position using newly collected material. All new materials were collected by the authors during different projects. In this study, the its systematic position of *M. cymuligera* are evaluated through an integrative approach based on multiple molecular datasets and morphological evidence. Phylogenetic analyses included plastid data comprising 83 protein-coding genes and four plastid regions, 352 low-copy nuclear genes, and nuclear ribosomal ITS and ETS sequences. Maximum Likelihood and Bayesian analyses of the plastid datasets consistently recovered *M. cymuligera* in association with *Mentha*, on the other hand the nuclear datasets produced conflicting topologies involving *M. cymuligera*, *Mentha*, and *Cyclotrichium*. Nevertheless, the combined molecular and morphological evidence supports *M. cymuligera* as a distinct evolutionary lineage within Menthinae. Morphologically, the species is characterized by an annual, non-rhizomatous habit, a resupinate corolla, two fertile and two sterile stamens with divergent thecae, and non-mucilaginous mericarps. In light of the congruent morphological, molecular, ecological, micromorphological, and cytological evidence, we recognize this lineage at generic rank and propose the new monotypic genus *Anatolia*, with the new combination *Anatolia cymuligera*.

Keywords: *Anatolia*, *Mentha*, Menthinae, Nepetoideae, Türkiye

Symposium 11- Mediterranean forests: Ecology & challenges

Chairs: Ünal Akkemik, Stephan Woodward

11.1 Stephan Woodward - Mediterranean forests under pressure: Climate change, biological invasions, and emerging risks to forest ecosystems

11.2 Candan Aykurt - Phylogenetic diversity patterns in mediterranean mountain plant communities: A case study from the Western Taurus Mountains (Türkiye)

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11.6 Deniz Aygören Uluer - A preliminary molecular phylogeny of the genus *Thalictrum*: Insights into Turkish taxa

11.1

Mediterranean forests under pressure: Climate change, biological ınvasions, and emerging risks to forest ecosystems

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Globally, Mediterranean forests are among the most biologically diverse and ecologically valuable ecosystems, yet they are increasingly threatened by the combined effects of climate change, biological invasions and escalating disturbance regimes. Rising temperatures, prolonged droughts, fires and more frequent extreme weather events are altering forest structure and function while facilitating the establishment, spread and impact of invasive pests and pathogens.

Climate-induced stress reduces tree vitality and resilience, increasing susceptibility to insect outbreaks and pathogen infections. At the same time, globalization and international trade have accelerated the introduction of non-native organisms into Mediterranean landscapes, creating novel ecological interactions and unprecedented risks for native biodiversity. Recent examples from the Mediterranean Basin, particularly from Türkiye, demonstrate how invasive alien species and climate-driven outbreaks of forest insects and pathogens including *Corythucha arcuata*, *Cydalima perspectalis*, *Anoplophora chinensis*, *Leptoglossus occidentalis*, *Ips typographus*, *Orthotomicus erosus*, and pathogens such as *Ceratocystis platani*, *Ophiostoma novo-ulmi*, *Diplodia* spp., *Dothistroma pini*, *Calonectria pseudonaviculata*, *Cryphonectria parasitica*, *Seridium cardinale*, *Heterobasidion annosum* sensu lato, and invasive/emerging *Phytophthora* species can trigger forest decline, disrupt ecosystem processes, and compromise essential ecosystem services.

In this presentation, we examine the interactions between climate change and forest pests and pathogens, emphasizing climate-driven range expansions, increased host susceptibility, and the synergistic effects of biological invasions, wildfires and post-fire ecosystem dynamics. Future risk scenarios and management challenges will be discussed, highlighting the importance of early detection, integrated surveillance, adaptive forest management, strengthened biosecurity and international cooperation. Particular attention will also be given to potential future threats to the Mediterranean region, including *Bursaphelenchus xylophilus, Fusarium circinatum*, and the frequently cryptic bacterial pathogen *Xylella fastidiosa*. Understanding these interactions is essential for developing effective conservation and silvicultural strategies that enhance the resilience of Mediterranean forests to climate change.

Keywords: Mediterranean forests; Climate change; Invasive forest pests; Forest pathogens; Ecosystem resilience; Adaptive forest management.

11.2

Phylogenetic diversity patterns in Mediterranean mountain plant communities: A case study from the Western Taurus Mountains (Türkiye)

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Mountain systems within the Mediterranean Basin are exceptionally rich in plant diversity and endemism due to their complex topography, microclimatic heterogeneity, and diverse habitat types [1; 2; 3]. These mountain ecosystems, recognized among the world's most important biodiversity hotspots [4], are currently under considerable threat from climate change and anthropogenic pressures [5; 6; 7]. Therefore, the development of effective conservation strategies is of great importance. In areas characterized by mosaic diversity patterns [8], the joint evaluation of different components of biodiversity may provide more robust and realistic insights for ecosystem sustainability. In this study, the phylogenetic structure of plant communities distributed along the Asıl Beydağları Mountains in the Western Taurus Mountains was investigated, and phylogenetic diversity values were compared with previously determined species diversity, functional diversity, and endemism values from the same study area.

A total of 973 seed plant species recorded from 136 sampling plots were used in the analyses. A phylogenetic tree was constructed using the V.PhyloMaker2 package and the GBOTB.extended.LCVP mega-phylogeny, and the majority of taxa were successfully integrated into the phylogenetic framework. The phylogenetic structure of communities was evaluated using the standardized effect size of mean pairwise distance (SES-MPD) metric.

The results indicate that the phylogenetic structure of plant communities in the Western Taurus Mountains varies across habitat types and vegetation belts. No significant phylogenetic clustering was detected within communities, whereas differences among habitats and vegetation belts were largely associated with patterns of phylogenetic overdispersion. Higher phylogenetic diversity values were observed particularly in the Supra- and Oro-Mediterranean vegetation belts and in the forest habitats occurring within these belts. Although a positive relationship was found between endemism and phylogenetic structure, no significant relationship was detected with species diversity or functional diversity. These findings suggest that different components of biodiversity in Mediterranean mountain ecosystems may exhibit complementary patterns. Our study further indicates that incorporating phylogenetic diversity into conservation planning may contribute to a more comprehensive evaluation of the evolutionary diversity of the Western Taurus Mountains.

Keywords: Mediterranean mountains, Phylogenetic Diversity, Plant communities, Vegetation belts, Western Taurus Mountains

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11.3

Mediterranean forests under changing fire regimes: Regeneration, resilience and emerging challenges

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Fire is a fundamental ecological process in Mediterranean ecosystems, shaping vegetation structure, species composition and plant functional strategies over evolutionary and ecological time. Mediterranean plant communities are characterized by a diversity of fire-persistence mechanisms [1], particularly resprouting and post-fire recruitment from persistent seed banks, whose relative importance varies among vegetation types and environmental conditions. Fire-related regeneration traits, including heat- and smoke-stimulated germination, further contribute to the capacity of many Mediterranean species to persist under recurrent fire [1].

The effectiveness of these mechanisms, however, depends on the characteristics of the fire regime and the conditions prevailing before and after fire. Fire severity and recurrence, pre-fire vegetation structure, drought, land-use history and post-fire management can all influence the direction and rate of vegetation recovery. Evidence from Turkish red pine (*Pinus brutia*) forests and Mediterranean shrublands in Türkiye indicates considerable potential for natural regeneration, while also demonstrating that post-fire interventions may alter recovery trajectories and, in some cases, provide little ecological advantage over natural regeneration.

Climate and land-use changes are now modifying Mediterranean fire regimes and increasing the likelihood of extreme fire events, creating conditions that may exceed the regeneration capacity of some ecosystems [2]. Consequently, rapid recovery of vegetation cover should not necessarily be equated with recovery of species composition, ecological functions or resilience to subsequent fires. Recognizing both the capacity and the limits of natural regeneration is therefore crucial for anticipating the future of Mediterranean forests and for developing management approaches that maintain biodiversity and ecological resilience under changing fire regimes.

Keywords: Climate change, Fire regime, Mediterranean forests and shrublands, Resilience, Wildfire.

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11.4

Genetics and conservation of native *Populus* and *Salix* species in Turkish riparian forests: Insights from nuclear SSRs and plastid barcodes

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Riparian vegetation across Mediterranean and Anatolian river basins is subjected to severe pressure from climate change, altered hydrological regimes, and habitat fragmentation. Within these ecosystems, members of the Salicaceae family—predominantly *Populus* and *Salix* species—serve key functions in soil stabilization, streamflow regulation, and habitat restoration. Despite their ecological and forestry significance, regional molecular data on genetic divergence, marker transferability, and plastid sequence variation remain sparse for Anatolian lineages. This study investigates the molecular relationships among six native taxa (*Populus nigra*, *P. alba*, *P. tremula*, *P. euphratica*, *Salix alba*, and *S. caprea*) collected from contrasting river basins in Türkiye.

A total of 149 trees were sampled from five major river systems (Tekirdağ, Dicle, Göksu, Çoruh, and Kızılırmak). Genomic DNA extraction followed a modified CTAB protocol. Molecular characterization relied on 12 nuclear microsatellite (SSR) loci alongside three plastid barcode regions (*matK*, *rbcL*, and *trnH-psbA*). Bidirectional Sanger sequencing data were aligned and concatenated to construct Maximum Likelihood and Neighbour-Joining trees in MEGA11.

Nuclear SSR analysis demonstrated clear intergeneric separation with minimal allele sharing between *Populus* and *Salix*. Loci WPMS05, PMGC2163, and PMGC93 amplified consistently across *Populus* taxa, confirming their cross-species transferability. High allelic diversity occurred in *P. tremula*, *P. nigra*, and *P. alba*, whereas *P. euphratica* displayed a lower and more restricted allelic profile. Plastid markers exhibited distinct substitution rates: *matK* yielded high species-level resolution, *rbcL* remained markedly conserved, and *trnH-psbA* recorded the highest nucleotide diversity ($\pi = 0.04$) and insertion/deletion frequency. Phylogenies based on concatenated plastid datasets confirmed *Populus* and *Salix* as monophyletic sister clades, positioning the stress-adapted *P. euphratica* as a distinct lineage sister to the remaining poplars. Integrating nuclear SSR fingerprinting with plastid barcoding resolves taxonomic boundaries and evolutionary relationships in Turkish Salicaceae. The observed genetic divergence in specialized taxa such as *P. euphratica* provides practical baseline information for germplasm preservation and seed transfer zone delineation in Mediterranean riparian restoration efforts.

Keywords: Mediterranean riparian forests, *Populus*, *Salix*, DNA barcoding, SSR markers, Systematics, Türkiye

11.5

The effect of climate change on some forest trees and their growth in the Mediterranean basin of Türkiye

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The Mediterranean basin is one of the regions most affected by climate change, an issue directly related to Türkiye. Climate change significantly affects trees, particularly the width of their rings, as well as their distribution. In this context, this paper aims to present how the tree-ring growth of the naturally occurring *Pinus brutia* Ten.[1] and *Pinus pinea* L.[2] species in the Aegean region is affected by climate change. A review based on two published articles on the subject was conducted, comparing the ways in which the tree-ring widths of these two pine species are affected. According to the results obtained, these two important tree species in the region have become distinctly dependent on precipitation. While the trees can tolerate increases in temperature, the primary limiting factor in tree growth is precipitation. However, increased evaporation and reduced humidity associated with high temperatures mean that current precipitation levels are insufficient. Consequently, tree-ring widths have become even more dependent on the water supply. This leads to the death of these trees, particularly under unfavorable conditions, resulting in widespread forest die-off, especially on south-facing slopes. In both the Aegean and Mediterranean regions of Türkiye, tree death is increasing, particularly on south-facing slopes and at lower altitudes. In the long term, afforestation with these species will continue in areas where soil conditions are favorable. However, in areas where conditions are unfavorable, it may be discussed to avoid afforestation and allow the area to revert to its natural maquis vegetation.

Keywords: *Pinus brutia, Pinus pinea*, Tree ring, Dendroclimatology, Tree death

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11.6

A preliminary molecular phylogeny of the genus *Thalictrum*: Insights into turkish taxa

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Thalictrum Tourn. ex L. is represented by 11 taxa in Türkiye and approximately 210 species worldwide. In the Flora of Türkiye, both the generic and species-level treatments are brief and insufficient, and the genus is characterized as 'very difficult.' In addition, unresolved synonymy and the lack of a comprehensive evaluation of infraspecific taxa have contributed to taxonomic uncertainty and frequent misidentifications. To address these issues, extensive fieldwork was conducted. Phylogenetic relationships were inferred using nuclear ITS and chloroplast *trn*L and *trn*L-F sequences generated in this study, together with sequences retrieved from GenBank, under Maximum Likelihood (ML) and Bayesian Inference (BI) approaches. The results provide a framework for improving the taxonomy and understanding the evolutionary history of *Thalictrum* in Türkiye, highlighting that the genus remains exceptionally challenging from both morphological and molecular perspectives. Nevertheless, the present work provides the first comprehensive molecular phylogenetic assessment of the genus *Thalictrum*, with a particular emphasis on Turkish taxa.

Keywords: Meadow-rue, Phylogeny, Ranunculaceae, Systematics, *Thalictrum*

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Symposium 12- Molecular studies may provide help to taxonomy

Chairs: Barış Özüdoğru, Christoph Oberprieler

12.1 Karol Marhold - Multiple hybrid zones involving four *Cardamine* species and their triploid progeny: Another nascent neopolyploids in action?

12.2 Dörte Harpke - A phylogenomic framework for understanding diversification, genome evolution, and karyotype changes in *Crocus*

12.3 Ozan Şentürk - Phylogenomic reassessment of the tribe Genisteae (Leguminosae): New insights into an iconic Mediterranean plant group

12.4 Maria Ángeles Alonso-Vargas - Molecular phylogeny of the genus *Frankenia* (Frankeniaceae): new evidence from Eurasia and Africa

12.5 Tim Böhnert - From topology to taxonomy: phylogenomics and genus delimitation in Mediterranean hyacinths

12.6 Ruifang An - Phylogenomics and cytogenetics reveal differentiated lineages in the *Crocus serotinus* complex

12.7 Jordi Lopez-Pujol - Molecular studies in support of taxonomy: examples from the Western Mediterranean basin

12.8 Emrullah Yılmaz - Genome wide RADseq data provide new insights into species boundaries in the *Noccaea densiflora* complex

12.1

Multiple hybrid zones involving four *Cardamine* species and their triploid progeny: Another nascent neopolyploids in action?

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Hybridization between species is a powerful evolutionary force that can lead to the exchange of genetic material, the formation of new species, and significant shifts in biodiversity. Hybrid zones, regions where genetically distinct populations meet and interbreed, offer unique opportunities to study these processes in real time. In particular, they provide insights into interspecific gene flow, introgression, genetic erosion, and the emergence of polyploid organisms, which have played a crucial role in plant evolution. One key mechanism of speciation in plants is allopolyploidization, where hybridization between species is followed by genome doubling, leading to the formation of new, reproductively isolated lineages. The genus *Cardamine* is an important model for this process, as it includes one of the few well-documented neo-allopolyploid species that have arisen within the last 300 years. In this study, we revealed an unprecedented case of extensive interspecific hybridization in *Cardamine*: a dynamic system of seven hybrid zones in the mountains of western Bulgaria, involving four parental species and their predominantly triploid offspring. Using a combination of flow cytometric screening, next-generation restriction site-associated DNA sequencing, and genomic in situ hybridization, we demonstrate the recurrent and polytopic origins of both autotriploids and allotriploids, with the latter integrating distinct parental genomes. Our findings highlight *Cardamine rivularis* as a central player in this system, likely due to its frequent production of unreduced female gametes, which drive the formation of diverse triploids. However, this species may also face the risk of genetic swamping and ecological displacement. While most triploid hybrids appear to belong to the F1 generation, their substantial genetic diversity, high frequency, and efficient clonal spread suggest significant evolutionary potential. Overall, we propose that these hybrid zones provide a rare and valuable natural laboratory for studying the emergence of neo-allopolyploid species and the broader mechanisms shaping polyploid evolution.

Keywords: Cruciferae, Hybrids, Flow cytometry, Restriction site-associated DNA sequencing, Genomic in situ hybridization

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12.2

A phylogenomic framework for understanding diversification, genome evolution, and karyotype changes in *Crocus*

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The genus *Crocus* L. (Iridaceae) is characterized by remarkable chromosome number variation, extensive dysploidy, and limited diagnostic morphological characters, resulting in unresolved phylogenetic relationships and persistent taxonomic uncertainty. We used a nested phylogenomic approach to resolve relationships across the genus. The backbone phylogeny was reconstructed using plastid genomes, 35S rDNA, and 14 nuclear single-copy genes, whereas genotyping-by-sequencing (GBS) was used to resolve relationships within more recently diverged lineages. Whole-genome duplication events were identified through analyses of gene duplications and synonymous substitution rates using 12 long-read genome assemblies. We detected an ancient whole-genome duplication (Cr-β) predates the origin of modern *Crocus* species, together with multiple additional lineage-specific duplication events. Comparative analyses suggest an allopolyploid origin for Cr-β involving the ancestors of *Afrocrocus* J.C.Manning & Goldblatt, *Syringodea* Hook.f., and *Crocus*. Our analyses indicate that the evolutionary history of several taxonomically challenging groups was shaped by rapid radiations, incomplete lineage sorting, and complex patterns of genome and chromosome evolution. Integrating phylogenomic, genomic, and morphological evidence explains why these groups have remained difficult to classify and identifies previously overlooked morphological characters that support several inferred relationships. These findings reshape our understanding of evolutionary relationships within *Crocus* and provide the basis for a comprehensive taxonomic revision of the genus.

Keywords: *Crocus*, Phylogenomics, Dysploidy

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12.3

Phylogenomic reassessment of the tribe Genisteae (Leguminosae): New insights into an iconic Mediterranean plant group

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The brooms, *Genista* L., *Cytisus* L. and allied genera (tribe Genisteae, Papilionoideae, Leguminosae), constitute a key physiognomic and ecological component of the Mediterranean Basin, with around 250 species [1]. For over two centuries, Genisteae has attracted considerable research interest because of its distinctive secondary metabolites, extensive polyploidy and complex patterns of diversification. Why, for example, are there many more narrowly circumscribed genera in the Mediterranean/European regions than in Southern Africa and the Americas, where relatively few genera contain similarly high, or even higher, species numbers? Despite extensive analyses based on morphological, chemical, and limited molecular markers, generic and subgeneric relationships have not been fully resolved, hindering our understanding of the classification of Genisteae as well as geotemporal patterns of diversification [2].

Here, we present preliminary results from a new phylogenomic analysis of Genisteae, with a particular focus on Mediterranean lineages in their global context. Sampling included more than 100 taxa selected to represent the morphological and taxonomic diversity of the group, together with representatives from across its distribution in Eurasia, Africa and the Americas. Using the Angiosperms353 target-enrichment probe set, we recovered hundreds of low-copy nuclear loci to investigate relationships across the tribe. The resulting phylogeny provides a framework for reassessing the classification of Genisteae and interpreting patterns of diversification across the Mediterranean Basin and adjacent regions.

Keywords: Angiosperms353, Genisteae, Mediterranean Basin, Phylogenomics, Systematics.

References:

[1] Bisby, F. A. *Advances in Legume Systematics*, 1981, 1, 409–425.
[2] Pardo, C. et al. *Plant Systematics and Evolution*, 2004, 244, 93–119.

Acknowledgment: We gratefully acknowledge financial support from the Sibbald Trust, Royal Botanic Garden Edinburgh (Project 2020#23), RBGE Expedition Fund (2024–2026), and the James & Eve Bennett Trust (2025).

12.4

Molecular phylogeny of the Genus *Frankenia* (Frankeniaceae): New evidence from Eurasia and Africa

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Recent phylogenetic studies of *Frankenia* have provided new insights into species delimitation and evolutionary relationships across Eurasia and Africa. These findings complement ongoing taxonomic research that has led to the reinstatement of previously overlooked species, (*Frankenia nodiflora*), and the recognition or description of additional taxa (*F. anneliseae*, *F. dinteri*, *F. sahariensis*, and *F. nummularia*). These studies favour understanding of species diversity and evolutionary patterns within one of the most challenging groups of halophilous plants in the Mediterranean and adjacent regions [1, 2].

This contribution focuses on two major aspects of *Frankenia* systematics. First, phylogenetic relationships among Macaronesian taxa (including the Azores, Canary, Cape Verde, Madeira, and Savage archipelagos) are clarified, along with their biogeographical connections to Africa. Attention is paid to the taxonomically complex aggregates of *F. ericifolia* s.l. and *F. capitata*, whose evolutionary relationships remain poorly understood. The resulting phylogenetic framework provides new evidence regarding patterns of diversification and dispersal within Macaronesia. Second, we focus on *F. hirsuta*, one of the most taxonomically controversial groups within the genus. Our analyses, together with the typification of the Linnaean *F. hirsuta*, facilitate resolution of relationships among close taxa that are frequently treated as synonyms in the latter, including *F. aucheri*, *F. bucharica*, and *F. salsuginea*. The results also support recognition of a new species, *F. aegyptica* M.Á. Alonso et al. (in press). Furthermore, the phylogenetic position of *F. revoluta* is examined in relation to the *F. hirsuta* group and the closely related *F. syrtica*, originally subordinated to *F. corymbosa*.

Biogeographical and taxonomical delimitation of the *F. hirsuta* complex highlights the need of further investigation on the *F. laevis* group. Current morphological and molecular evidence consistently supports recognition of two well-defined lineages within this complex: a western Mediterranean lineage corresponding to *F. intermedia* and an Atlantic lineage attributable to *F. laevis* sensu stricto.

Keywords: *Frankenia*; ITS phylogeny; Typification; Linnaean plant names, Plant taxonomy

References:

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[2] Alonso, M.Á. et al. *Plants*, 2025, 14(7), 1130.

12.5

From topology to taxonomy: Phylogenomics and genus delimitation in Mediterranean hyacinths

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Scilla s.l. has long represented one of the most problematic genus complexes among Mediterranean bulbous geophytes. Numerous segregate genera have been proposed on the basis of morphology, cytology, seed characters, and phenology. However, limited molecular resolution and incomplete taxon sampling have so far prevented a robust evaluation of these competing generic concepts. Here, we present a densely sampled phylogenomic framework for Hyacinthinae (Scilloideae/Hyacinthaceae) based on Angiosperms353 target-capture data, including nearly all historically recognized genera and roughly one third of the lineage's species diversity [1]. Orthology-aware filtering and complementary concatenation and coalescent analyses recover a robust backbone and confirm that *Scilla* s.l. is polyphyletic, with several widely accepted genera such as *Hyacinthus*, *Muscari*, and *Bellevalia* deeply embedded within the broader *Scilla* complex. The resulting topology resolves a series of well-supported, morphologically coherent lineages corresponding largely to historically proposed segregate genera. Remaining conflict is restricted to a few nodes, particularly within the *Hyacinthus*-alliance, and likely appear to reflect rapid early divergence and/or ancient reticulation. Integrating phylogenomic evidence with morphology and cytology therefore supports a revised genus-level classification recognizing 20 genera in Hyacinthinae. Beyond its taxonomic implications, this study illustrates how phylogenomics can inform robust and biologically meaningful classifications in Mediterranean plant systematics.

Keywords: Angiosperms353; Target capture; Scilloideae; Integrative taxonomy; Classification

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12.6

Phylogenomics and cytogenetics reveal differentiated lineages in the *Crocus serotinus* complex

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The Iberian autumn-flowering *Crocus serotinus* complex combines unstable taxonomy and overlapping morphology [1] with variable chromosome counts ($2n$ = 22, 24, 44 and 48) [2]. Divergence time estimation based on plastome and 35S rDNA data dated the origin of the *C. serotinus* complex to ca. 3.5 Ma. Species delimitation in such recent plant radiations is complicated by shallow divergence and reticulation. We sampled 106 populations of the focal complex and three outgroup populations and integrated genome-wide genotyping by sequencing (GBS) data with plastid and rDNA markers, flow cytometric genome-size estimates, SNP-ratio profiles, chromosome counts, fluorescence in situ hybridization (FISH) and repeat composition analyses. Although GBS generated a sufficient number of SNPs, the phylogeny remained partly unresolved, likely reflecting the challenges of resolving evolutionary relationships in the presence of allopolyploids. As a consequence, a conservative assessment using multiple ploidy indicators was applied to identify polyploids and diploids, resulting in the retention of 65 populations classified as diploid. Six major diploid genomic lineages, all separated by fully supported internal nodes in the SVDQuartets tree, were recovered. Fixation index values ranged from 0.248 to 0.691, showing substantial but uneven differentiation. Analyses of shared and private alleles further supported their separation. Plastid *ycf1* and rDNA relationships did not fully match those inferred from the genome-wide SNP data, indicating discordance among marker systems that was likely caused by incomplete lineage sorting. Cytogenetic analyses revealed differences in chromosome number ($2n$ = 22 or 24) and variation in FISH signal patterns, even when chromosome counts were the same. Differentiation among the six diploid lineages was further supported by differences in repeat composition and genome size. Although the studied complex represents a recent radiation, these results are consistent with the presence of six differentiated diploid evolutionary entities within the *C. serotinus* complex, including two potential new species.

Keywords: *Crocus serotinus*; Species delimitation; Genotyping-by-sequencing; Cytonuclear discordance; Chromosome variation

References:

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12.7

Molecular studies in support of taxonomy: Examples from the Western Mediterranean basin

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The western Mediterranean Basin is itself a biodiversity hotspot, harboring thousands of native plant taxa, including numerous narrow endemics. However, plant taxonomy in this region remains particularly challenging due to its complex geological history, high habitat heterogeneity, and ongoing evolutionary processes, which often blur traditional species boundaries. This issue is especially relevant in a region facing intense anthropogenic pressures and where the impacts of climate change are expected to be particularly severe. As a result, many plant taxa are currently threatened with extinction and require effective conservation measures. A well-resolved taxonomy is a prerequisite for the inclusion of taxa in regional or national lists of threatened and endangered species, thereby enabling the implementation of conservation actions such as recovery plans. Since the late twentieth century, the advent of molecular tools—often combined with ecological niche modelling—has revolutionized taxonomy, which was traditionally based primarily on morphological evidence, with unforeseen consequences for the legal protection and practical conservation of plant taxa. Here, we present several examples drawn from some of the most emblematic elements of the western Mediterranean flora, illustrating how molecular approaches have reshaped traditional taxonomic concepts and the resulting conservation and legal implications. Specifically, we examine the Iberian endemic genus *Petrocoptis* (with particular emphasis on the pair *P. montsicciana–P. pardoi*), *Cynara baetica* and its subspecific entities, and the pair *Lobularia maritima* subsp. *maritima*/*L. maritima* subsp. *columbretensis*).

Keywords: Conservation, Endemic species, Genetic markers, Species delimitation.

12.8

Genome-wide RADseq data provide new insights into species boundaries in the *Noccaea densiflora* complex

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The *Noccaea densiflora* complex is among the most taxonomically challenging groups of the genus, because the morphological characters traditionally used for species delimitation, including fruit shape, style length and the position of the style between the apical notches, vary considerably and overlap among the currently recognised taxa. Earlier analyses based on a limited number of nuclear and plastid markers provided insufficient resolution to clarify these boundaries. Here, we used Restriction Site-Associated DNA Sequencing (RADseq) data from 59 individuals sampled across the geographical and morphological range of the complex in Türkiye. Population genetic structure was investigated using principal component and ancestry analyses. In parallel, a reproducible Snakemake-based workflow was developed to recover, filter and rank RAD loci for locus-wise and coalescent-based phylogenomic inference. After filtering, 95,859 high-confidence SNPs were retained, while 500 of the most informative loci were selected from 3,722 aligned loci for species-tree reconstruction. The SNP-based analyses revealed pronounced genomic structuring, broadly separating populations assigned to *N. microstyla* and *N. violascens*, while also identifying intermediate or admixed populations. The multilocus species tree largely recovered the same principal lineages and indicated the distinct evolutionary position of the geographically isolated Engize population. Taken together, these results appear most compatible with a comparatively broad three-species framework comprising *N. microstyl*a, *N. violascens* and *N. haussknechtii*. Within this interpretation, populations traditionally assigned to *N. amani* and *N. densiflora* may represent geographically and morphologically differentiated elements of the broader *N. microstyla* and *N. violascens* lineages rather than independently evolving species. More broadly, the strong correspondence between SNP-based population structure and multilocus phylogenomic inference demonstrates that the newly developed pipeline can provide substantial resolution in a species complex that had remained largely unresolved with conventional molecular markers. By revealing a genomic pattern broadly consistent with the recognition of *N. microstyla*, *N. violascens* and *N. haussknechtii*, this approach offers a practical framework for translating high-resolution molecular evidence into a more coherent taxonomic treatment.

Keywords: Brassicaceae; Phylogenomics; RADseq; Species delimitation; Taxonomy

POSTERS

P1

Exploring the cultivable fungal diversity of turkish propolis samples and their bioactivities

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Propolis is a bee-derived natural product known for its complex chemical composition and important role in hive defense. While its chemical composition and biological activities have been extensively investigated, recent studies have revealed that propolis also harbors a diverse microbiome. However, the fungal diversity associated with propolis and its potential as a source of bioactive microorganisms remain largely unexplored [1, 2]. Propolis samples were collected from seven ecologically distinct provinces of Türkiye (Antalya, Artvin, Balıkesir, Bilecik, İzmir, Konya, and Sivas) from hives separated by at least 5 km to capture regional diversity. Fungal isolation was performed using five culture media: Potato Dextrose Agar, Czapek Dox Agar, Malt Extract Agar, Malt Yeast Agar, and Sabouraud Dextrose Agar. A total of 300 fungal isolates were recovered. No significant differences were observed among the culture media in terms of isolate recovery ($p > 0.05$). When normalized, Balıkesir exhibited the highest fungal recovery with 32 isolates per hive, followed by Artvin (20.3 isolates), whereas Antalya yielded the lowest recovery. Later, representative fungal isolates with distinct colony morphologies were selected for analytical-scale fermentation and preliminary antimicrobial screening. In parallel, raw propolis samples were analyzed using ITS-based metabarcoding to characterize microbial diversity. The findings indicate that propolis collected from diverse ecological regions of Türkiye harbours a rich cultivable fungal community and represents a promising source of bioactive microorganisms for natural product discovery. The combined use of fungal isolation, bioactivity screening, and metagenomics-based analyses provides complementary insights into the diversity and biotechnological potential of propolis-associated fungi.

Keywords: Propolis, Mycobiome, Metagenomics

References:

[1] Sallemi, S. et al. *Evid Based Complement Alternat Med.*, 2022, 16.
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P2

The role of lichens in astrobiology and astrobotany: A guide to the basic literature

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Lichens are one of nature's most resilient mutualistic partnerships, formed between a heterotrophic fungus (mycobiont) and a photosynthetic alga and/or cyanobacteria (photobiont). This symbiotic coordination gives lichens an extraordinary ability to withstand extreme environmental conditions that a single organism could not tolerate. Recent astrobiology research has shown that lichens can challenge space conditions such as high UV radiation, cosmic rays, extreme temperature fluctuations, and vacuum through extremophilic adaptations. This review article comprehensively examines the strategic importance of lichens in astrobiology, extremophile biology, and future astrobotany applications. First, the role of lichens in the lithopanspermia theory predicting interplanetary life transfer and their survival success in space simulation experiments are discussed. Second, the metabolic resilience mechanisms they exhibit in extreme analogous environments like Mars are analysed from an extremophile biology perspective. Finally, the potential of lichens in astrobotanical applications as pioneer organisms (biomarkers and soil-forming organisms) in future exoplanet colonisations and Martian terraphosformation processes is discussed. In conclusion, lichens stand out as one of the most powerful model organisms not only for Earth but also for challenging space missions and extra-terrestrial habitation scenarios. Unravelling this multifaceted symbiosis will open new horizons for future astrobotany and synthetic biology studies.

Keywords: Astrobiology, Astrobotany, Lichen, Extremophiles, Space Simulation

P3

Assessing the representativeness of the MA Herbarium: Taxonomic and geographic coverage of the Iberian flora

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Herbaria are fundamental repositories for documenting plant diversity, yet the representativeness of their collections is rarely assessed quantitatively. The Herbarium of the Real Jardín Botánico (MA) houses nearly one million specimens. Approximately 65% originate from the Mediterranean region, while 55% of the entire collection corresponds to the Iberian flora (including Spain, Portugal and the Balearic Islands), making MA the world's largest herbarium collection for this region.
Taxonomic coverage was assessed by comparing the Iberian checklist (ca. 7,500 native and introduced taxa) with the digitized Iberian specimens preserved at MA. Geographic representativeness was assessed at the provincial level by comparing the number of taxa represented in MA with the number of taxa recorded for each province in *Flora Iberica*, together with patterns of collecting intensity.
The herbarium contains specimens for almost all Iberian taxa, with only about 250 taxa currently unrepresented. Most missing taxa correspond to cryptic narrow endemics, recently introduced alien species, extremely rare native plants and extinct taxa.
The floristically richest regions are generally well represented in MA, but geographic representation is uneven, with some species-rich areas, particularly those encompassing the Pyrenees, comparatively underrepresented. Historical collecting patterns show that 52% of the analysed Iberian specimens were collected between 1982 and 2020, during the Flora Iberica period. This approach provides an objective assessment of the strengths and gaps of one of the largest Mediterranean herbaria and offers a framework for guiding future digitization, collection development and targeted field sampling.

Keywords: Herbarium collections; Iberian flora; Taxonomic coverage; Geographic representativeness; Collection bias; Floristic completeness

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P4

The BC Herbarium as a resource for Mediterranean flora research

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The BC Herbarium of the Botanic Institute of Barcelona (CSIC-CMCNB) is the second largest botanical collection in Spain, housing more than 800,000 specimens. It constitutes a major repository of plant biodiversity and an essential source of information for studying the flora of the Mediterranean Basin. In addition to its continuously growing collections of vascular plants and cryptogams—including bryophytes, lichens, fungi and algae—the herbarium preserves 14 historical collections (dating from the 17th century to the beginning of the 20th century). It also contains specialized collections maintained separately because of their nature or origin, such as a xylotheque, a spermatheca, a tissue bank and collections of cultivated plants.

The BC Herbarium combines historical and contemporary material, providing a unique temporal perspective on Mediterranean plant diversity and distribution. Through ongoing digitization efforts, part of its collections is accessible to researchers worldwide through online databases, while physical specimens remain available for consultation through loans, research visits and curatorial services. Consequently, the herbarium has become a key resource for a broad range of scientific disciplines, including taxonomy, systematics, floristics, phylogeny, biogeography, evolutionary biology, conservation, ethnobotany, biological invasions and global change research [1].

In this contribution, we provide an overview of the specimens from the Mediterranean Basin preserved at the BC Herbarium, highlighting the taxonomic, geographic and historical breadth of the collections. We also present a selection of remarkable specimens that illustrate the scientific value of herbarium collections beyond their traditional role as repositories of preserved plants. These examples demonstrate how the BC Herbarium continues to support innovative research and contributes to our understanding and conservation of Mediterranean plant diversity in the face of current environmental challenges.

Keywords: Cryptogams; Herbarium specimens; Mediterranean Basin; Plant collection applications; Vascular plants.

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P5

The Biblical Herbarium of Father Ubach: A unique botanical collection from the Sinai and the Holy Land

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Father Bonaventura Ubach (*1879–†1960) was a Benedictine monk of the Montserrat Abbey (Catalonia, Spain) who assembled an extraordinary and unpublished plant collection during his travels through the Holy Land and other regions of the Levant in the early 20th century. His aim was to illustrate and explain the landscapes, life and traditions described in the Bible.

Nowadays, Father Ubach's biblical herbarium takes part of the Montserrat Museum and is a unique and exceptional collection due to its original purpose. The plants' origins (Sinai and the Holy Land), the label annotations (localities, biblical passages, and vernacular names), and the time of its formation make this collection a valuable source of taxonomic, floristic, historical, and phytonymic data. This collection, however, has gone virtually unnoticed to date, so an integral study of all its botanical aspects is gravely needed. As a first step, Father Ubach's biblical herbarium has been digitized to ensure its online accessibility and it will be subjected to a minimal restoration to ensure its long-term preservation.

The next step will be the systematic revision of the herbarium which will lead to an improvement in taxonomic and nomenclatural knowledge and may even lead to the identification of new taxa. This revision, together with the study of Father Ubach's original manuscripts and notes, will also improve the floristic knowledge of the places he visited (the Sinai Peninsula but also the Holy Land). This might let us expand the current geographic range of some plant species, detect places where certain species have become extinct and, in general, evaluate the changes in the vegetation and landscapes since the time Father Ubach visited the area. This information may prove vital in the context of ongoing climate change and the current biodiversity extinction crisis in an area where there are hardly any studies of this type.

Keywords: Biblical collections; Biblical plants; Sinai; Holy Land; scientific collections.

P6

Beyond preservation: From herbarium Wolnyanum (1797) to #SrbijaCveta2026

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Herbaria are recognized not only as repositories of preserved specimens but also as dynamic resources supporting biodiversity research, education, conservation, and public engagement. Historical collections frequently reveal that botanical knowledge has long depended on collaboration between naturalists and local communities. A notable example is the ampelographic collection of the Herbarium Wolnyanum, completed in 1824 by unknown author [1, 2], which relied extensively on local vine-growers, illustrating how botanical knowledge emerged through interactions between scientists and society.

Drawing inspiration from this legacy, the national citizen science initiative #SrbijaCveta2026 explores how herbaria can extend their role beyond specimen preservation by integrating public participation, biodiversity monitoring, and digital documentation. The project engages citizens in documenting the distribution and flowering phenology of vascular plants through georeferenced photographic observations, creating a nationwide network of contributors. Participants submit georeferenced photographs of vascular plants through social media platforms and dedicated project channels, while species identifications are verified by botanists before incorporation into the database.

By integrating community-generated observations with institutional botanical collections into the BUNS herbarium digital infrastructure, #SrbijaCveta2026 contributes valuable ecological information while promoting botanical literacy and public awareness of plant diversity. During the first five months of the project, participants documented nearly 1,000 vascular plant species occurring in Serbia, demonstrating the remarkable potential of citizen involvement in biodiversity monitoring. The initiative has reached a broad audience, attracting approximately 50,000 online views per month and an expanding network of contributors throughout Serbia. Most participants are not professional biologists but nature enthusiasts of diverse ages and backgrounds, highlighting the broad societal interest in plant diversity and environmental stewardship.

The rapid growth of #SrbijaCveta2026 demonstrates that the participatory spirit of botanical documentation remains relevant today. By integrating citizen-generated observations with institutional collections, the project demonstrates how herbaria can function as repositories of botanical heritage, sources of contemporary biodiversity data, and platforms for public engagement.

Keywords: Herbaria; Participatory botany; Citizen science; Botanical heritage; Serbia

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NOT PRESENTED

P7

Genus *Verbascum* (Scrophulariaceae): An updated checklist and integrated reassessment of the species richness

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As part of an ongoing project focused on taxonomic and nomenclatural revisions of the genus *Verbascum* L. worldwide [1], the present study offers a critical inventory and thorough reassessment of specific diversity within the group for the first time. This updated checklist was based on fieldwork; examination of relevant plant material in several herbaria or by contacting the relevant curators; and revision and compilation of existing literature, including studies or annotations that might provide data from regional and local floras, catalogs, checklists, monographs [2], articles, doctoral or master's dissertations, and more reliable floristic electronic databases. Reliable online taxonomy websites were used for nomenclature revision and to collect more data about type, bibliographical citations in the original publications, names, and synonymies. Each taxon name was verified under the guidance of the International Code of Nomenclature for algae, fungi, and plants. Endemism status was established using existing literature and online databases. The genus' taxonomic history is reviewed, and a global distribution map is presented. The update checklist includes a total of 510 accepted taxa, comprising 467 species and 43 subspecies. Among these, 321 taxa, representing 62%, are classified as strict endemics, existing solely within specific locations or regions defined by the current political boundaries of countries. Additionally, a total of 525 synonyms have been listed. Recent outnumbers revealed that the genus's specific diversity, previously assessed to 360–400, was underestimated. The higher number of endemic taxa with 191 taxa (ca. 63% of all endemic taxa in genus and ca. 38% of all taxa in the genus) is found in the Irano-Turanian region (in particular, Türkiye and part of Iran). However, there is two secondary centers of diversity in circum-mediterranean areas, the first one encompasses the Balkan and Italy, where 54 endemic species of *Verbascum* occur and the second secondary center is located in the western Mediterranean basin including the Iberian Peninsula and Morocco with about 40 native species, of which 18 are endemic. On the other hand, two endemic species-rich regions could be considered, one in the north part of Eastern Africa with 10 species and the other is located in the Arabian Peninsula with 15 species. Some new combinations are proposed here (*Verbascum longirostre* subsp. *antiatlanticum* (Emb.) Khamar (≡ *Celsia longirostris* var. *antiatlantica* Emb.), *V. longirostre* subsp. *atlanticum* (Maire) Khamar (≡ *Celsia longirostris* var. *atlantica* Maire), *V. longirostre* subsp. *hoggaricum* (Maire) Khamar (≡ *Celsia longirostris* var. *hoggarica* Maire), *V. maroccanum* subsp. *lanuginosum* (Maire) Khamar, (≡ *Celsia maroccana* f. *lanuginosa* Maire) and *V. orientalum* (L.) Khamar (≡ *Celsia orientalis* L). This updated inventory will serve as a crucial reference and basis for further floristic research, biodiversity monitoring, phylogeny, and conservation planning within the genus.

NOT PRESENTED

Keywords: Center of diversity, Endemism, Genus *Verbascum*, New combination, Species list, Taxonomy.

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NOT PRESENTED

P8

Morpho-anatomical, micromorphological, and palynological characterization of *Verbascum bugulifolium*: Implications for taxonomy and evolutionary adaptations

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Verbascum bugulifolium, commonly referred to as "Riva mullein," is a rare species with a limited distribution in northwestern Türkiye. In the Flora of Türkiye, Huber-Morath classifies *V. bugulifolium* within group A as synonymous with *Celsia bugulifolia* [1]. Specimens collected from Istanbul were subjected to examination using both light and scanning electron microscopy. Morphological, anatomical, and palynological analyses identified glandular hairs with heads comprising 1–2 cells and stalks consisting of 2–10 cells, as well as multicellular-headed glandular hairs in the stem and basal leaf sections. The dorsiventral structure of the basal leaf and the reniform vascular bundle were confirmed through light microscopy, while electron microscopy revealed covering and glandular hairs on the leaf surfaces. Palynological studies involved quantitative measurements of pollen under a light microscope using the Wodehouse method, while surface ornamentation was observed with a scanning electron microscope. Contrary to literature [2] that reports a single pollen type, heteromorphy was observed: 50% of the pollen was tricolporate, 40% tetracolpate, and 10% tricolpate. This structure facilitates rapid germination from tetracolpate pollen while providing resistance to water loss, indicating potential for hybridization and adaptive reproductive strategies. Moreover, the capsule is broadly ellipsoid, measuring 5–8 × 4–6 mm, and densely covered with glandular and covering hairs. Seeds are oblong-ovate prismatic, dark brown to black, measuring 0.79–0.82 × 0.88–1.07 mm, and exhibit a deeply alveolate structure under electron microscopy. This comprehensive biosystematic study offers crucial data for the taxonomic differentiation and understanding of the evolutionary adaptations of *V. bugulifolium*.

Keywords: *Verbascum bugulifolium*, Mullein**,** Anatomy, Pollen, Micromorphology.

References:

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P9

One further step toward the resolution of *Valerianella* and *Valeriana* confusion: Evolutionary relationships of little-known *Valerianella* species support the current taxonomy

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The genus *Valerianella* is a taxonomically complex genus of medium size. Phylogenetically, some North American species and a limited number of Eurasian species have been analysed and form a nested lineage within the paraphyletic genus *Valeriana*, together with the genus *Fedia*. It is accepted as a synonym for *Valeriana* in some current databases. In this study, the evolutionary relationships of all *Valerianella* species distributed in Türkiye were revealed by studying trnK-matK intron, psbA-trnH inter-genetic spacer, and internal transcribed spacer (ITS1-5.8S rDNA-ITS2) markers for 74 populations belonging to 32 species, 22 of which were phylogenetically studied here for the first time. Consistent with the literature, the genus *Valerianella* was found to be nested in the paraphyletic lineage of *Valerianella* together with *Fedia*. Excluding *Cornigerae* and *Sclerocarpae* sections, it was concluded that the studied sections are not monophyletic, the current intraspecific classification is therefore not natural. *Platycoele* and *Siphonocoele* sections are polyphyletic, while *Coronatae*, *Physocoele* and *Locustae* sections are paraphyletic. Most of the species studied with multiple populations did not form monophyletic lineages. New species complexes have been added to those recorded to date to reflect the existence of fruit polymorphism without phylogenetic separation. *V. turgida* were added to *V. locusta + V. carinata* complex; *V. vesicaria, V. obtusiloba, V. lasiocarpa, V. chlorostephana, V. kotschyi* and *V. hirsutissima* were added to *V. coronata + V. pumila* complex. *V. muricata* was included in *V. dentata + V. rimosa* complex. Additionally, *V. cymbicarpa* and *V. plagiostephana* constitute a new species complex. In addition, the species *V. discoidea, V. glomerata, V. uncinata, V. oxyrhyncha* and *V. echinata* have been shown to be monophyletic.

Keywords: *Valeriana*, *Fedia*, Phylogeny, Türkiye

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NOT PRESENTED

P10

Biodiversity within the *Centaurea busambarensis* Complex (Asteraceae, Cardueae) in Sicily

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Sicily is one of the main centres of diversification of the genus *Centaurea* L. in the Mediterranean Basin, harbouring a remarkable diversity of endemic taxa [1]. Within the *Centaurea cineraria* aggregate (sect. *Centaurea*), the *Centaurea busambarensis* complex is one of the most taxonomically challenging groups.

Recent taxonomic studies [2] have progressively increased the recognised diversity of this complex through the description of three additional species, mainly occurring in the coastal mountain ranges of central-western Sicily. To date, this complex comprises twelve specific and infraspecific taxa on the island. In addition to the nominal species (*C. busambarensis Guss.*), it includes *C. aegusae* Domina, Greuter & Raimondo, *C. erycina* Raimondo & Bancheva, *C. panormitana* Lojac. subsp. *panormitana*, *C. panormitana* subsp. *ucriae* (Lacaita) Greuter, *C. saccensis* Raimondo, Bancheva & Ilardi, *C. seguenzae* (Lacaita) Brullo, Marcenò & Siracusa, *C. todaroi* Lacaita, *C. tyrrhena* C. Brullo, Brullo & Giusso, *C. valdemonensis* Domina, Di Grist. & Barone, *C. haluntina* Gianguzzi, Di Grist., Barone & Domina.

Further field investigations in the Trapani Mountains have revealed populations that are distinct from the taxa previously described from this part of the island, highlighting the importance of this area as a centre of diversification for both the *Centaurea busambarensis* complex and the genus as a whole.

Ongoing taxonomic analyses, based primarily on diagnostic morphological characters and supported by ecological and chorological differences, indicate that two new species can be distinguished among the populations occurring in the Trapani area. Molecular analyses are currently underway, focusing on the species of the complex occurring in western Sicily, to clarify the genetic relationships among the taxa under investigation.

Keywords: Taxonomy, Endemic species, Floristic diversity, Mediterranean Basin

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P11

Pollen, fruit, and seed micromorphology of *Hedysarum* subsect. *Subacaulia* (Fabaceae) taxa from Türkiye with taxonomic implications

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The family Fabaceae, comprising roughly 19,500 species across 751 genera, is recognized as the third-largest flowering plant family, exhibiting remarkable species diversity and evolutionary success across diverse global ecosystems [1-2]. Represented by approximately 225 species of annual or perennial herbs, the genus *Hedysarum* L. is widely distributed throughout temperate Eurasia, Northern Africa, and North America [3]. In Türkiye, 33 taxa of *Hedysarum* have been recognized to date [4]. The present study evaluates the palynological, carpological, and seed micromorphological characteristics of *Hedysarum* subsect. *Subacaulia* taxa distributed in Türkiye to elucidate their systematic and taxonomic significance. Diagnostic features were investigated using both Light Microscopy (LM) and Scanning Electron Microscopy (SEM). Qualitative and quantitative measurements were obtained via the Kameram 21 software attached to a Leica DM 1000 light microscope with a Canon EOS 450D camera. Multivariate statistical analyses (including PCA and Cluster Analysis) were conducted in R to evaluate character variations. Our results indicate that pollen size, muri dimensions, and exine ornamentation, alongside fruit and seed surface architecture, provide highly effective diagnostic characters for species discrimination. Consequently, the combination of palynological and micromorphological traits plays a crucial role in accurately delineating and classifying the investigated members of subsect. *Subacaulia*.

Keywords: Cluster analysis, Leguminosae, Pollen analysis, SEM, Sweet-vetch.

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P12

Contributions to the taxonomy of *Polygonum setosum* and *Polygonum luzuloides* (Polygonaceae/Polygonoideae) inferred from palynological and molecular data

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Polygonum setosum Jacq. and *Polygonum luzuloides* Jaub. & Spach have been treated as separate species in some national floras [1,2], where as they have been treated as subspecies under the *P. setosum* (*P. setosum* subsp. *setosum and P. setosum* subsp. *luzuloides*) [3,4]. In this study, several plant samples from Türkiye belonging to the two taxa were examined in terms of their morphological, palynological, and molecular characteristics. While *P. luzuloides* is characterised by erect and robust stems, broadly lanceolate leaves with revolute margins, and a verrucate fruit surface, *P. setosum* has ascending to erect, numerous and slender stems, linear to linear-lanceolate leaves, flat leaf margins, and a smooth fruit surface. Similarly, *P. luzuloides* has subprolate pollen grains, whereas *P. setosum* is characterized by spheroidal pollen grains. ITS sequence data supported the recognition of *P. luzuloides* and *P. setosum* as distinct species, with both recovered in well-supported clades. The integrative morphological, palynological, and molecular evidence presented in this study supports the recognition of *P. luzuloides* and *P. setosum* as distinct species rather than as taxa at the infraspecific rank.

Keywords: *Polygonum*, Pollen, Taxonomy, Türkiye

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P13

A comparative study on *Hieracium karakolense* and *Hieracium medianiforme*

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Hieracium L. (hawkweed), which is in Cichorieae (Lactuceae Cass.) Lam. & DC. tribe of the Asteraceae Bercht. & J. Presl family, is represented by 117 species in our country according to the latest literature, with the 63% endemism rate [1]. Polyploidy, apomixis, and hybridization lead to significant taxonomic and nomenclatural confusion within the genus [2]. In Türkiye, the genus *Hieracium* is represented by 14 series. Among these, the series *Pseudopannosa* stands out due to its high species richness, 100% endemism rate, and severe taxonomic complexities. Taxa belonging to this group are presumed to have arisen from hybridization events between Ser. *Pannosa* and alternative series. During our field studies in the Kastamonu (Karakol region), we observed and collected two species, *Hieracium karakolense* (Borum. & Zahn) Sell & West and *Hieracium medianiforme* (Litw. & Zahn) Juxip, both of which were originally collected by Bornmüller and had long remained uncollected from this area. Morphological similarities between the two species were noted during field observations. This study aims to clarify the distinctions between the two species by comparing their morphological, anatomical, and palynological characteristics. In this context, morphological features were investigated using a stereomicroscope. Moreover, the stem and leaf anatomy, as well as the pollen morphology of the two *Hieracium* taxa, were examined in detail via light microscopy. Some differences were observed in several characteristics, including stem length, trichome density, and capitulum number. Nevertheless, further molecular studies are required to provide more definitive evidence regarding the distinctions between these two species, thereby resolving the taxonomic confusion. This study represents a small step toward understanding the taxonomic complexity of the genus *Hieracium* and is hoped to pave the way for future research.

Keywords: Asteraceae, Anatomy, LM, Pollen, Systematic

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P14

Taxonomic analysis of a critical Sicilian population of *Anthemis* (Asteraceae, Anthemideae)

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In Sicily, as in other Italian regions, the family Asteraceae is particularly rich in genera and species, some of which are taxonomically complex and include critical groups. In the Mediterranean flora, this is especially evident in *Centaurea* L., *Hieracium* L., *Taraxacum* F.H. Wigg. and *Anthemis* L. (1). Several taxa have recently been described or rediscovered, particularly in Sicily.
Anthemis includes numerous annual and perennial species in Sicily, the latter belonging to sect. *Hiortia*. Classical works reported *A. aetnensis* Spreng. on the volcanic substrates of Mount Etna; *A. cretica* subsp. *columnae* (Ten.) Frazén in dry stony meadows, often on limestone; *A. cupaniana* Tod. ex Nyman on shady limestone cliffs and screes in the Madonie and Palermo Mountains (C-N Sicily); and *A. ismelia* Lojac. on limestone cliffs at Monte Gallo (Palermo).
More recently, *A. messanensis* Brullo on schistose cliffs of the Peloritani Mountains (N-E Sicily); *A. pignattiorum* Guarino, Raimondo & Domina on limestone cliffs in the Hyblaean Mountains (S-E Sicily); and *A. parlatoreana* Raimondo, Bajona, Di Gristina & Spadaro in the carbonate ranges of the Castellammare Mountains (N-W Sicily) have been added to the Sicilian flora.
Here, we present and analyse a critical population clearly differentiated from the other species of sect. *Hiortia* occurring in Sicily and the Mediterranean region (1–2). It is relatively isolated and occurs on scattered carbonate outcrops within the clayey landscape of central Sicily, under thermo-xerophilous conditions. The associated phytocoenosis mainly comprises *Prasium majus* L., *Silene fruticosa* L., *Ruta chalepensis* L., *Euphorbia dendroides* L., *Melica ciliata* L., *Athamanta sicula* L., *Umbilicus rupestris* (Salisb.) Dandy, *Ceterach officinarum* DC, *Ballota rupestris* (Biv.) Vis., *Rhamnus alaternus* L., *Chamaerops humilis* L. and *Pistacia terebinthus* L. Phytosociologically, the population plays a differential role in a phytocoenosis attributable to *Asplenietalia glandulosi* Br.-Bl. & Meier 1934.
Based on its indumentum and morphological characters, including narrow, elongated leaf lobes, commonly uniflorous scapes, involucral bracts, and absence of papillae on the achenes, the population exhibits sufficient diagnostic characters to support its recognition at species level.

Keywords: Biodiversity, vascular flora, taxonomy, endemism, Sicily.

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P15

Deriving more data: Use of elliptic fourier analysis to assess capsules in closely related *Crocus* taxa

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Crocus is a taxonomically complex genus whose relationships are not clearly delimited and often poorly defined due to their extreme variability and overlapping morphological and anatomical traits. Often an extreme amount of multi-disciplinary data is necessary to obtain clear results from analyses between taxa, and for this reason creative use of different measurement and analysis techniques is paramount to advancing studies of this genus. Fruit features are underutilized in crocuses because of difficulty acquiring material, natural variation and relative dearth of features commonly used to describe them, which is usually limited to categorical descriptions of shape and color while dimensions are subject to variation depending on pollination and ecological factors. To test the potential of using morphometric tools to produce more sensitive shape data, we conducted an Elliptic Fourier Analysis on 150 capsules from 40 populations of *C. chrysanthus s.l.* taxa collected from Türkiye, where the *Crocus chrysanthus* species complex is represented by 13 taxa. These include species, subspecies and varieties whose relationships are not yet clearly understood, making it a suitable case study for assessment of this technique. Fruits were collected from the field in early summer or raised in cultivation after collection at anthesis. After being photographed using a herbarium digitization system using a color scale with ruler, the fruits were visually inspected, removing underdeveloped and dehisced capsules from the analysis. Elliptic Fourier Analysis was performed in Morphological Analysis of Size and Shape (MASS) software using 10 harmonic coefficients. The resulting coefficient and measurement data were used to conduct PCA analyses in PAST 4. Significant differences between morphometric fruit features and mean outline shapes were observed using this method, making it a valuable tool to generate large amounts of numeric and measurement data for analysis in variable and difficult to assess species.

Keywords: Contour analysis, Morphometrics, Fruit morphology

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P16

Macro- and micromorphological properties of capsules and seeds of the endemic *Fumana grandiflora* and *Fumana trisperma* (Cistaceae) from Türkiye

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The genus *Fumana* Spach (Cistaceae) comprises 18 species worldwide, of which 10 occur in Türkiye, two of which are endemic [1,2]. In this study, the macro- and micromorphological characteristics of the capsules and seeds of endemic *Fumana grandiflora* Jaub. & Spach and *Fumana trisperma* Hub.-Mor. & Reese from Türkiye were investigated using light microscopy (LM) and scanning electron microscopy (SEM) to provide detailed morphological data and to evaluate their taxonomic significance. Plant materials were collected from their natural populations. For each species, at least 30 mature capsules and seeds were examined under a stereomicroscope, photographed, and measured for length and width. Prior to SEM examination, the capsules and seeds were cleaned in a 1:1 (v/v) ethanol–xylol solution, mounted on aluminum stubs using double-sided adhesive tape, and sputter-coated with gold. Micromorphological observations and imaging were performed with a FEI INSPECT F50 SEM [3]. Capsules are loculicidal, 3-valved, yellowish-brown, and triangularly ovoid, measuring 3.20–5.00 mm in length and 3.00–4.60 mm in width, with sparse to dense, cream-colored simple trichomes at the carpel apices. The seed numbers per capsule differed among the investigated *Fumana* species (*F. grandiflora* 5–6(-7) seeds, *F. trisperma* 3 seeds). The capsule surface exhibits a scalariform ornamentation pattern in both species. Seeds are brown to blackish-brown, trihedral, ovoid, 2.10–3.10 × 1.20–2.10 mm, with a suture running from the chalaza to the apex and ending in a small beak. The seed coat ornamentation is reticulate-striate in *F. grandiflora*, but colliculate in *F. trisperma*. Variation in capsule size, seed numbers per capsule and seed coat ornamentation provides reliable evidence for distinguishing the examined *Fumana* species. The present study highlights the diagnostic value of fruit and seed macro- and micromorphological characters in species delimitation and offers a valuable foundation for future systematic investigations within the genus *Fumana*.

Keywords: *Fumana*, Fruit, Seed, SEM, Türkiye

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P17

Lectotypification of *Stachys trinervis* (*Stachys*, sect. *Ambleia*)

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Stachys L. is one of the largest genera of Lamiaceae, comprising approximately 370 species distributed mainly in temperate and subtropical regions of the Northern Hemisphere. Section *Ambleia* Benth. represents a morphologically distinctive lineage characterized by a suffruticose perennial habit, dendroid indumentum, xerophytic adaptations, and predominantly 2–6-flowered verticillasters [1]. The section comprises 12 species and 13 taxa worldwide, with its distribution centred in the Irano-Turanian and eastern Mediterranean phytogeographical regions.

Stachys trinervis Aitch. & Hemsl. was described by Aitchison and Hemsley in 1886 from the Hari-rud Valley of Afghanistan based on the gathering J. E. T. Aitchison 157. Although the name has been consistently accepted in subsequent floristic and taxonomic treatments, no lectotype has ever been designated. Examination of the protologue and original material revealed that the name was published without indication of a holotype. Original specimens attributable to the type gathering were traced in the herbaria K, G, and GH.

Detailed comparison of the original material showed that the specimen preserved at the Royal Botanic Gardens, Kew (K000928703) bears the original collection label, analytical pencil sketches illustrating diagnostic morphological characters, and a copy of the original protologue attached to the herbarium sheet. These features indicate that the specimen was closely associated with the taxonomic study of the species and represents the most informative original material currently available. Accordingly, the specimen K000928703 is designated as the lectotype of *Stachys trinervis*, whereas the specimens preserved at G (G00435958) and GH (GH00002082) are treated as isolectotypes in accordance with the International Code of Nomenclature for algae, fungi, and plants (Shenzhen Code).

This lectotypification stabilizes the application of the name *Stachys trinervis* and provides a nomenclatural framework for future taxonomic studies of *Stachys* sect. *Ambleia*.

Keywords: *Lectotypification, Lamiaceae, nomenclature, Stachys, sect. Ambleia*

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P18

Cancel culture? The differences between leaf anatomy in in-situ and ex-situ *Crocus* accessions

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Because of their life cycle that often features hysteranthus vegetation and extended dormancy, *Crocus* L. specimens are frequently taken into cultivation for observation throughout the year. This provides researchers with ongoing access to various plant parts, including root tips, flowers, leaves, fruits and seeds. Leaf anatomic features rank amongst the most commonly trusted characters employed in systematic studies in the genus and many studies record the shape and size of the carina, number and features of the vascular bundles and arms, cell and cross-section height and width, lacuna and white stripe area and their proportions to leaf dimensions for use in descriptions and datasets. However, studies about the extent to which abiotic factors influence these data are lacking even though many researchers use ex-situ material for publication of new species. In our ongoing studies, we noticed salient differences between *Crocus* leaf cross sections from field-collected specimens and the same specimens from our ex-situ collections. Knowing that key differences in some morphological features, have been observed in cultured specimens, we set out to assess how leaf anatomy can differ between in-situ and ex-situ leaf samples from the same population. We selected 13 *Crocus chrysanthus* s.l. populations, from which 3-6 leaves were taken each from the field and live collections grown in containers for 1-2 years. Plant samples were embedded in paraffin, sectioned using a manual microtome and stained using Safranin-Alcian Blue double stain before photographing and measuring in a digital environment. The results were stark: cultured plants showed much higher variation overall, while field-grown samples were more similar to each other, even across species boundaries, than they were to the same specimen's potted individuals. The results once again highlight the importance of using field-collected material in new species descriptions and standard treatment of all samples to be used in combined datasets.

Keywords: Phenotypic plasticity, Morpho-anatomy, Iridaceae

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P19

Micromorphological Examination of Some *Ajuga* L. (Lamiaceae) Species in Türkiye

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This study provides a detailed SEM-based investigation of the micromorphological characteristics of various organs, including the stem, abaxial and adaxial leaf surfaces, calyx, corolla, filament, and nutlet, in five *Ajuga* species naturally distributed in Türkiye: *A. bombycina* Boiss., *A. genevensis* L., *A. reptans* L., *A. iva* (L.) Schreb., and *A. laxmannii* (Murray) Benth. The observations revealed the presence of simple unicellular and multicellular non-glandular trichomes on the stems, abaxial and adaxial leaf surfaces, calyces, corollas, and filaments of most species. In contrast, such trichomes were not observed on the stem or on either leaf surface of *A. reptans*. Subsessile, short-stalked, and long-stalked capitate glandular trichomes were also generally observed among the investigated species. Nutlet analyses showed that the nutlets were elongated-oblong to oblong-ovoid in *A. bombycina* and *A. iva*, ovoid to obovoid in *A. genevensis* and *A. reptans*, and ovoid to oblong-ovoid in *A. laxmannii*. Regarding nutlet surface ornamentation, *A. bombycina* and *A. genevensis* exhibited rugose-reticulate patterns, *A. reptans* showed a coarsely reticulate pattern, and *A. laxmannii* displayed a finely reticulate pattern. In contrast, the transversely ridged-rugose surface observed in *A. iva* represents a particularly distinctive and potentially valuable taxonomic character.

Keywords: *Ajuga*, endemic, micromorphology, Lamiaceae, Türkiye

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P20

Comparative anatomy of selected *Ajuga* taxa from Türkiye and its taxonomic significance

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This study presents a comparative anatomical investigation of the roots, stems, and leaves of seven *Ajuga* taxa distributed in Türkiye: *A. laxmanii*, *A. reptans*, *A. genevensis*, *A. relicta*, *A. vestita*, *A. xylorrhiza*, and *A. iva*. Plant materials were embedded in paraffin, sectioned, stained with Safranin–Fast Green, and mounted as permanent slides. The preparations were examined under a light microscope, and 30 measurements were taken for each quantitative anatomical character in each taxon. Although the taxa shared a broadly similar anatomical organization, clear differences were observed in tissue structure, thickness, and the number of cell layers. In the roots, an epidermis was present in *A. laxmanii*, *A. reptans*, and *A. genevensis*, whereas a periderm was observed in *A. relicta*, *A. vestita*, *A. xylorrhiza*, and *A. iva*. The root cortex consisted of 5–16 cell layers, the sclerenchyma of 1–7 layers, and the phloem of 5–18 layers; notably, sclerenchyma was absent in *A. iva*. Root phloem thickness ranged from 105.96 to 338.49 µm, with the highest value recorded in *A. xylorrhiza*. The stems generally exhibited the quadrangular structure characteristic of Lamiaceae, while the numbers of cortical, collenchymatous, sclerenchymatous, and phloem layers varied among the taxa. *Ajuga relicta* was distinguished by its 9–10-layered collenchyma and the greatest stem phloem thickness (50.46 µm). All taxa had bifacial leaves, with the mesophyll differentiated into palisade and spongy parenchyma. The palisade parenchyma generally consisted of 2–3 layers, whereas 3–4 layers were observed in *A. relicta*. Mesophyll thickness ranged from 174.81 to 276.78 µm, with the highest value recorded in *A. genevensis* and the lowest in *A. reptans*. The midrib generally contained a single large central vascular bundle, whereas one or occasionally two large vascular bundles were observed in *A. genevensis*. Overall, the type of protective tissue and the development of sclerenchyma and phloem in the roots, variation in supporting and vascular tissues in the stems, palisade parenchyma and mesophyll characteristics of the leaves, and vascular organization of the midrib were among the most informative anatomical features for distinguishing the examined taxa. The results indicate that the combined assessment of qualitative and quantitative anatomical characters provides useful complementary evidence for the identification and taxonomic evaluation of *Ajuga* taxa distributed in Türkiye.

Keywords: *Ajuga*, Endemic, Anatomy, Lamiaceae, Türkiye

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P21

Micromorphology and anatomy of *Poa jubata* (Poaceae)

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Poa jubata A. Kern (gömü salkımotu) is a rare and short-lived species endemic to Southeastern Europe. According to the Euro+Med Plantbase database, this taxon is limited to Albania, Bulgaria, Croatia, Greece, and the Thrace region of Türkiye. The Flora of Europe and Flora of Türkiye (Edmondson, 1980, 1985) indicate that this species prefers dune and coastal habitats, but its taxonomic proximity to other species is not specified. Because *P. jubata* (gömü salkımotu) differs significantly morphologically and molecularly from other *Poa* species identified to date in Europe and worldwide, it has been evaluated under a separate section. Furthermore, two new locations have been identified for this taxon, and its morphology and habitat preferences have been re-evaluated. The species is described in detail and illustrated, and its relationships are discussed.

This study fills a gap in the literature and provides an opportunity for comparison with other taxa in terms of micromorphology and anatomy.

Keywords: Anatomy, Annual habit, Flora, Habitat, Micromorphology.

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P22

Stem and leaf anatomy of *Fallopia* species (Polygonaceae) native to Türkiye

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Fallopia Adans. (Polygonaceae) is a genus comprising approximately 13 species, some of which are recognized worldwide for their invasive characteristics. The genus is represented in Türkiye by two native taxa, *Fallopia convolvulus* (L.) Á.Löve and *F. dumetorum* (L.) Holub. The present study aimed to examine the stem and leaf anatomy of two native *Fallopia* species in order to assess their taxonomic significance for species delimitation. Sections were prepared from plant materials preserved in ethanol (70%) using a freezing microtome and freehand sectioning, and examined under a light microscope. Both taxa are characterized by ridged stems supported by collenchyma, a continuous sclerenchyma ring, bifacial hypostomatic leaves, calcium oxalate druses, and multicellular peltate glandular hairs. Although both taxa shared a similar stem and foliar anatomy, they differed in several quantitative anatomical characters, as follows: *F. convolvulus* exhibited a thicker cortex (41.2 ± 7.9 µm), sclerenchyma (100.4 ± 9.9 µm), stem vascular bundles (174.1 ± 41.4 µm), midrib vascular bundles (178.1 ± 25.5 µm), and mesophyll (176.4 ± 16.6 µm), together with larger stomata (25.6 ± 2.3 × 33.8 ± 2.5 µm) and epidermal cells (47.7 ± 10.8 × 84.1 ± 20.7 µm), and a higher stomatal index (21.7 ± 2.6). In contrast, *F. dumetorum* was characterized by a thinner cortex (30.2 ± 9.1 µm), sclerenchyma (63.6 ± 20.4 µm), stem vascular bundles (133.1 ± 40.3 µm), midrib vascular bundles (89.5 ± 14.7 µm), and mesophyll (111.9 ± 13.1 µm), as well as smaller stomata (18.9 ± 2.3 × 26.4 ± 11.8 µm) and epidermal cells (40.6 ± 11.8 × 64.7 ± 14.3 µm), and a lower stomatal index (17.6 ± 3.3). This study provides anatomical evidence supporting the delimitation of *F. convolvulus* and *F. dumetorum*.

Keywords: Anatomy, *Fallopia*, Light microscopy, Türkiye

P23

New contributions to ChromoDB and OPTIMA publications: Expanding a curated, traceable database for plant chromosome counts

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As a parallel development of CromoCat [1], ChromoDB is a new curated chromosome database designed to improve the critical information on plant karyological data, often incomplete or inconsistent in current global repositories. The project offers a centralized, accessible, up-to-date resource for the global research community, building a reliable and traceable database for evolutionary, biogeographical, and conservation studies. It is available at https://chromodb.net/

Key features of ChromoDB include:

- ***Data quality and standardization*:** taxonomic normalization against POWO, expert validation, and a confidence level assigned to each record.
- ***Traceability*:** every record linked to its original publication via DOI or URL.
- ***Open and interoperable*:** versioned datasets published on Zenodo with a unique DOI, following FAIR principles, accessible via the ChromoDB.net portal.

Project viability was first validated through a pilot study on the journal *Lagascalia* (complete series up to 2024: 2,450 records corresponding to 1,120 taxa) [2]. Subsequent additions included: a) *Chromosome Numbers of Flowering Plants* by Fedorov et al. (1969), with over 79,000 individual chromosome counts and more than 8,000 bibliographic references (fully transliterated from the original Russian), and b) nearly 1,700 bibliographic references from the IAPT/IOPB chromosome data series (IOPB Chromosome Number Reports, IOPB Chromosome Data, and IAPT/IOPB Chromosome Data). We now present the recent inclusion of data from OPTIMA publications: a) *Flora Mediterranea* (2,811 records, 2,089 taxa, 50 countries, 296 references) and b) *Bocconea* (1,013 records, 726 taxa, 31 countries, 60 references). Current confidence level: 99.67%, with 100% verified originals [July 1, 2026]. The current version of ChromoDB offers more than 140,540 publicly searchable records. ChromoDB – The Global Chromosome Number Project has officially begun its integration into the GBIF infrastructure, following an agreement with the GBIF Spain unit (GBIF.ES) in Madrid.

Keywords: Chromosome counts, Biodiversity database, ChromoDB, CromoCat, GBIF

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P24

Filling in the blanks: New chromosome counts for five endemic *Crocus* species from Türkiye

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Karyological data is an important component of *Crocus* taxonomy and is especially important in Türkiye, a major center of diversity featuring innumerable narrow endemics and ongoing diversification that results in cryptic taxa and species complexes with muddy taxonomic boundaries. Ongoing speciation has a direct effect on the proliferation in recent years of newly published species and infraspecific taxa, particularly in the mountainous southwestern regions of Anatolia. Because of a relative lack of stable morpho-anatomical features, chromosome number is critical, alongside molecular, anatomical and morphological data to aid in the delimitation of difficult to define taxa in this genus. Despite the known importance of chromosome counts in *Crocus* systematics, the mad rush to publish new taxa before other researchers often means many new species are published without critical data, including primarily chromosome and molecular data. This, coupled with incomplete specimens and unclear diagnoses, means that many of these new taxa are at best imperfectly known, and at worst, fall into the nomen dubium category right at the starting line. This not only casts doubt on new species but hampers ongoing work to resolve relationships in this complicated genus. In the interest of filling in data holes left behind by taxonomists, we present for the first time chromosome counts along with idiograms and karyograms, for 5 narrow endemics from Türkiye: *C. gembosii* Rukšāns, *C. harpkeae* Rukšāns, *C. kerndorffiorum* Pasche, *C. taseliensis* Kernd. & Pasche, *C. crewei* Hook.f.

Keywords: Karyology; Iridaceae; Türkiye

NOT PRESENTED

P25

Visualizing chromosomal rearrangements: FISH evidence of centromeric telomere signals in Western Anatolian *Crocus* taxa

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The *Crocus chrysanthus* Herb. species complex is a systematically challenging group notable for its morphological variation and high cytogenetic diversity. Beyond traditional methods, molecular cytogenetic approaches are needed to elucidate the mechanisms behind the speciation processes of the taxa within this complex and understand the cause of their high plasticity. This study investigates the genome size, chromosome number and idiograms of two closely related taxa from Western Anatolia: *C. chrysanthus* subsp. *punctatus* F. Candan & Özhatay, here represented by populations in Kütahya (type locality) and İzmir, and *C. uschakensis* Rukšāns from its type locality in Uşak. At least 16 slides per population and 3 to 10 metaphase spreads from these slides were examined and mapped using DAPI. Three spreads were chosen for fluorescence *in situ* hybridization (FISH) and marked with genus-specific 45S rDNA, 5s rDNA and telomere probes. Successfully hybridized spreads were then photographed under fluorescent microscope. We found that *Crocus chrysanthus* subsp. *punctatus* has chromosome numbers of 2n=2x=20 and genome sizes of 2C=10.96 & 11.21, while *C. uschakensis* has 2n=2x=12 chromosomes and a genome size of 2C= 5.23. The chromosome counts for both taxa differed from those published in previous studies. FISH analysis detected telomere signals in the centromeric regions of all populations. This localization of telomere sequences, which are normally found at the ends of chromosomes, suggests that an evolutionary history characterized by major chromosomal rearrangements. Although more chromosomal landmarks, supported by molecular evidence, are needed to confirm these results, this study presents the first physical evidence of such phenomena in this group.

Keywords: Iridaceae, Chromosome, FISH

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P26

Genome size of Bulgarian species of *Scrophularia* (Scrophulariaceae)

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The genus *Scrophularia* is represented by seven species in the Bulgarian flora, united in two sections: *S.* sect. *Scrophularia* – *S. aestivalis*, *S. nodosa*, *S. scopolii* and *S. umbrosa*, and *S.* sect. *Tomiophyllum* – *S. bulgarica*, *S. canina*, *S. heterophylla* subsp. *laciniata*. Of these, *S. aestivalis* and *S. bulgarica* are Balkan endemics, while the others have a wider geographical distribution. In recent years, there has been growing interest in studying the phytotherapeutic properties of the species of the genus, as some of them have been used in folk medicine since ancient times. In this regard, a project is underway to conduct a comprehensive study of the genus in the Bulgarian flora, including the study of the chemical composition of the species, assessment of their potential as anti-obesogenic agents, as well as the accumulation of new biosystematic data and clarification of the phylogenetic relationships between taxa.

This poster presents genome size data for all seven *Scrophularia* species in the Bulgarian flora. The study was performed using flow cytometry. *Pisum sativum* 'Kleine Rheinlaenderin' (1C = 4.38 pg) was used as an internal standard for the measurements. The genome size of the Bulgarian representatives ranges from 1C = 0.61 pg for *S. heterophylla* subsp. *laciniata* to 1C = 0.79 pg for *S. aestivalis*. So far, genome size data has been published for only two of the species – *S. heterophylla* and *S. nodosa*, but for territories outside Bulgaria, and they are similar to the results of the present measurements, while the data for the other species are reported for the first time.

Keywords: Bulgarian flora, C-value, Flow cytometry, *Scrophularia*

Acknowledgment: Financial support of the Bulgarian National Science Fund under project '*A comprehensive study of the genus Scrophularia (Scrophulariaceae) in the Bulgarian flora – phytochemistry, biosystematics and anti-obesogenic activity*', Contract КП-06-Н79/6 of 05.12.2023, is gratefully acknowledged.

P27

Cytological investigation of two endemic *Ajuga* Species, *Ajuga postii* and *A. relicta* (Lamiaceae)

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The genus *Ajuga* L., commonly known as "Mayasıl otu" in Türkiye, has traditionally been used in folk medicine for pain relief and the treatment of hemorrhoids [1,2]. Belonging to the family Lamiaceae (subfamily Ajugoideae, tribe Ajugeae), the genus comprises 69 species and five hybrids, with a wide distribution across Europe, Asia, Africa, and Australia [3].

The most distinctive morphological feature of the genus *Ajuga*, which includes annual, perennial, and shrub-like taxa, is the structure of the corolla. The corolla may be either one-lipped or two-lipped. In the one-lipped form, the upper lip is extremely reduced or vestigial, whereas the lower lip is three-lobed, with the middle lobe being the largest. In the two-lipped form, both the upper and lower lips are well developed; the upper lip is two-lobed, while the lower lip is three-lobed. In rare cases, the upper lip is flat and the lower lip is four-lobed, with the middle lobe occasionally bifid [4,5]. Furthermore, a ring of hairs (annulus) is generally present inside the corolla tube.

In the present study, the endemic *Ajuga postii* and *Ajuga relicta*, were investigated cytogenetically. Methodologically, root-tip meristems were obtained by germinating the seeds on moist filter paper in Petri dishes at room temperature. The root tips were pretreated with α-monobromonaphthalene for 16 h at 4°C and subsequently fixed in a freshly prepared 3:1 (v/v) solution of absolute ethanol and glacial acetic acid. The fixed material was hydrolyzed in 1 N HCl for 11 min at room temperature and stained with 2% aceto-orcein for 2 h. The stained root tips were squashed in a drop of 45% acetic acid, and permanent slides were prepared using Depex mounting medium.

Chromosome measurements were performed using BS200ProP Image Analysis software. Karyotype parameters were determined from well-spread metaphase plates, and ideograms were constructed by arranging the chromosomes in descending order of their total length.

Cytogenetic analyses revealed that both *Ajuga postii* and *Ajuga relicta* possess a somatic chromosome number of 2n = 32. Detailed karyotype analyses were subsequently carried out for both taxa.

Keywords: *Ajuga*, Endemic, Karyotype, Lamiaceae, Türkiye

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P28

Comparative pollen morphology of endemic *Tanacetum alyssifolium* and its closely relatives *Tanacetum praeteritum* (Asteraceae) from Türkiye

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The genus *Tanacetum* L. (Asteraceae) is one of the largest and most taxonomically significant genera within the tribe Anthemideae, comprising approximately 150–160 species worldwide [1,2]. The objective of this study is to provide a detailed palynological characterization of the endemic *Tanacetum alyssifolium* (Bornm.) Grierson and the closely related endemic taxa *T. praeteritum* (Horwood) Heywood subsp. *praeteritum* and *T. praeteritum* (Horwood) Heywood subsp. *massicyticum* Heywood based on light microscopy (LM) and scanning electron microscopy (SEM), and to clarify the systematic importance of pollen morphological properties. Plant specimens used in the present study were collected from the type localities in Türkiye between 2023 and 2024. Pollen morphological analyses were performed using LM and SEM. Pollen slides for LM were prepared according to Wodehouse's method [3] and measurements were obtained from at least 50 pollen grains for each morphological parameter. For SEM analysis, pollen grains were mounted on stubs, sputter-coated with gold, and examined with a FEI INSPECT F50 scanning electron microscope. The pollen grains of *Tanacetum* taxa investigated are radially symmetrical, isopolar, and generally trizonocolporate (also tetracolporate type in *T. alyssifolium*). They exhibit a oblate-spheroidal shape, with the polar axis ranging from 25 to 43 µm and the equatorial axis measuring 25–45 µm. All taxa examined share an echinate exine ornamentation, whereas the sculpturing of the inter-spinal areas varies between taxa. A rugulate-perforate pattern is characteristic of *T. praeteritum* taxa, while *T. alyssifolium* is distinguished by granulate-perforate inter-spinal ornamentation. Pollen dimensions, aperture characteristics, and inter-spinal exine ornamentation were identified as the most informative palynological characters for discriminating among the examined *Tanacetum* taxa. The findings of this study are expected to provide valuable insights for future systematic studies of other *Tanacetum* taxa and to demonstrate the taxonomic significance of pollen characters in species delimitation.

Keywords: Asteraceae, *Tanacetum*, Pollen, Endemic, SEM

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P29

Palynological investigations on selected *Centaurea* species

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Centaurea L., which is in Cardueae (Lactuceae Cass.) tribe of the Asteraceae family, is represented by about 222 taxa in our country according to the latest literature, with the 60% endemism rate [1]. The fact that the endemism rate is so high in our country indicates that Türkiye is one of the important gene centers for the genus [2]. The main aim of this study is the palynological characterization of some *Centurea* taxa from Sect. *Centurea* and *Acrocentron*. In this context, the pollen morphology of 10 taxa of *Centurea* was researched in detail by light microscopy and scanning electron microscopy (SEM). Pollen grains were found as isopolar, radially symmetrical, and their shapes varied from oblate-spheroidal to subprolate. Tricolporate pollen grains were observed in all studied taxa. Different types of ornamentation (scabrate, microechinate-perforate) were identified in the SEM study. Some pollen characteristics, including pollen shape and ornamentation, showed significant differences between species. It is hoped that this study will be useful for understanding the relationships among *Centaurea* taxa and will provide guidance for future taxonomic studies.

Keywords: Asteraceae, LM, Pollen, SEM, Systematic

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P30

Authentication of commercial chestnut honeys via melissopalynological analysis

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Chestnut honey is an economically valuable monofloral honey in Türkiye due to its unique sensory profiles (1). This study investigated the botanical origin of eight commercial chestnut honey samples from various marketing channels using melissopalynological analysis combined with organoleptic evaluations.

Melissopalynological analyses revealed that the proportion of *Castanea sativa* Mill. pollen ranged from 1.0% to 98.5% among the examined samples. Seven of the eight samples contained dominant levels of *Castanea sativa* pollen (71.0–98.5%), fulfilling the criteria for monofloral chestnut honey. In contrast, one sample contained only 1% chestnut pollen and showed no palynological evidence supporting the botanical origin declared on the label. In addition, low proportions of pollen from *Tilia, Crataegus, Corylus, Quercus*, Fabaceae, Asteraceae, and Brassicaceae taxa were detected, indicating that honeybees also utilized a variety of surrounding floral resources. Samples containing high proportions of *Castanea sativa* pollen received higher sensory scores, demonstrating a positive relationship between chestnut pollen content and organoleptic quality. PCA revealed distinct clustering patterns among the honey samples according to their pollen composition, highlighting the significant contribution of pollen spectra to the observed variation among samples.

In conclusion, 87.5% of the commercial honey samples analyzed met the criteria for monofloral chestnut honey, whereas 12.5% were inconsistent with their label claims. The findings confirm that melissopalynological analysis is a reliable and effective tool for the authentication of chestnut honey and emphasize its importance in market surveillance, consumer protection, and quality control (2). Furthermore, the study contributes valuable data on the pollen diversity associated with Turkish chestnut honeys and demonstrates the usefulness of integrating palynological and sensory analyses for comprehensive honey characterization.

Keywords: Chestnut honey, *Castanea sativa*, melissopalynology, pollen analysis, honey authenticity

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P31

DNA barcoding of medicinal and aromatic plants from Artvin, Türkiye: Establishing a national reference dataset

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Medicinal and aromatic plants have high economic and strategic value due to their increasingly widespread use in the food, pharmaceutical, cosmetic, and phytotherapy industries. However, this growing demand has also increased concerns related to species misidentification, adulteration, mislabeling, and quality control. Therefore, accurate species identification of plant-derived products is essential for ensuring consumer safety, product authenticity, and the sustainable use of biological resources. DNA barcoding is one of the most effective and internationally recognized methods for the reliable molecular identification of species, enabling the verification of product authenticity, supporting quality control, preventing adulteration and fraud, and ensuring the traceability of plant-derived products. In this study, approximately 80 medicinal and aromatic plant species belonging to 72 genera and 38 families, naturally distributed in the flora of Artvin and of significant economic importance, were molecularly identified using DNA barcoding. Reliable reference sequences for the ITS, matK, and rbcL barcode regions were generated for economically, medicinally, and conservation-important taxa, including *Galanthus woronowii, Ruscus aculeatus, Cyclamen parviflorum, Hypericum bupleuroides, Crataegus turcicus, Valeriana* spp., and *Origanum vulgare*. The resulting sequences were submitted to the NCBI GenBank and BOLD Systems databases, thereby contributing to the strengthening of Türkiye's national DNA barcode infrastructure for medicinal and aromatic plants and enriching international reference databases. The reference dataset generated in this study provides a valuable scientific resource for quality control, species authentication, biodiversity conservation, the certification of geographical indication (GI) products, and the traceability of plant-derived products.

Keywords: Artvin, medicinal and aromatic, DNA barcoding, Türkiye

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Reassessment of the occurrence of *Crepis alpestris* in Türkiye based on morphological and molecular evidence

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Crepis alpestris (Jacq.) Tausch is a perennial herb widely distributed in Europe and is morphologically closely related to the polymorphic *C. conyzifolia* (Gouan) A. Kern. The presence of *C. alpestris* in Türkiye is based on the specimens *Pichler s.n.* and *Boiss s.n.* (ibid), collected from Uludağ (Bursa) lacking mature achenes, and these records were first reported in Flora Orientalis, later included by Babcock [1], and subsequently listed in the Flora of Türkiye [2]. Babcock [1] considered its record from Türkiye noteworthy, as the species is mainly distributed in Central Europe. Within the scope of revisionary studies on the genus *Crepis*, Uludağ has been revisited by several researchers, and new specimens morphologically resembling the *Pichler* s.n. specimen have been collected. The collected specimens were subject to detailed morphological comparisons with material from the herbaria B and KTUB, and specimens available in the K virtual herbarium. In addition, DNA was extracted from the recollected Uludağ specimens and from *C. conyzifolia*, and the ITS region was sequenced. These newly generated sequences, together with sequences retrieved from the NCBI database, were used in molecular phylogenetic analyses. The results of the analyses revealed that the specimens collected from Uludağ nested clearly within the *C. conyzifolia* clade and distant from the European *C. alpestris* samples. Morphological evidence also supports these findings; although the *Pichler s.n.* specimen lacks mature achenes, its achene-to-phyllary ratio is consistent with *C. conyzifolia* rather than *C. alpestris*. Furthermore, the achenes of the Uludağ specimen (*Coşkunçelebi & Güzel 1121*) are beakless and exhibit 15–20 ribs, which are characteristic features of *C. conyzifolia*. Considering all morphological, molecular, and geographical evidence, the only record of *C. alpestris* from Türkiye is erroneous and corresponds to *C. conyzifolia*. Therefore, it is concluded that *C. alpestris* is not distributed in the flora of Türkiye.

Keywords: *Crepis conyzifolia*, Molecular phylogeny, ITS, Uludağ

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P33

In silico approaches to the phylogenetic and taxonomic assessment of endemic monotypic genera and relict taxa in the flora of Türkiye

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Türkiye lies at the intersection of the Mediterranean, Irano-Turanian and Euro-Siberian phytogeographical regions and contains 11466 vascular plant taxa, approximately 31.8% of which are endemic [1]. Endemic monotypic genera and relict taxa represent unique evolutionary lineages, yet their nomenclature, generic boundaries and molecular data coverage remain uneven. This study evaluates the contribution of in silico approaches to the phylogenetic and taxonomic assessment of these lineages through an integrative review of the national flora, current nomenclatural databases, published molecular and phylogenomic studies, and publicly available sequence data. Endemism and monotypy were treated as distinct attributes, and selected genera, including *Vuralia* Uysal & Ertuğrul, *Oreopoa* H.Scholz & Parolly, *Cyathobasis* Aellen, *Thurya* Boiss. & Balansa, *Pseudophleum* Doğan, *Aegokeras* Raf. and *Microsciadium* Boiss., were assessed for nomenclatural stability, available molecular data, population sampling, voucher traceability, monophyly testing and nuclear-plastid congruence. The description of additional species has removed the monotypic status of *Pseudophleum* and *Aegokeras*. *Vuralia turcica* provides a particularly informative case: phylogenomic analysis based on 1,540 low-copy nuclear genes and complete plastomes clarified its biogeographical significance as a relict lineage, while also questioning its generic delimitation and revealing cytonuclear discordance [2]. For many other genera, molecular evidence remains restricted to DNA barcodes or a few loci, and population-level sampling and nuclear genomic resources are limited or absent. We therefore propose a staged workflow comprising nomenclatural auditing, construction of a taxon-by-data-type matrix, sequence quality control, multilocus phylogenetic and species-tree analyses, species delimitation, nuclear-plastid comparisons, and integration of phylogenetic distinctiveness with conservation priority. In silico analyses should guide, rather than replace, field, herbarium and laboratory studies, and direct limited resources toward taxa with the greatest uncertainty and evolutionary value. A versioned national checklist and voucher-linked genomic inventory are essential for documenting and conserving Türkiye's unique plant lineages.

Keywords: Endemic genera, Integrative taxonomy, Phylogenomics, Relict taxa, *Vuralia turcica*

References:

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P34

Characterization of *Melaleuca* Specimens from a Historical Botanical Garden in Southern Tuscany (Italy)

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The Corsini Botanical Garden is a historical garden founded in 1868 by Vincenzo Ricasoli nearby Porto Ercole (Tuscany), with the aim of acclimatizing valuable tree plant species originating from tropical areas. The historical collection includes species belonging to genera *Eucalyptus*, *Melaleuca*, *Acacia* and several genera of Palmae, together with a lot of other species that were imported and cultivated in the garden for more than a century. In the contest of an EU-PNRR garden requalification project, one of the crucial aims was to check the identity of the historic collection of plants in the park and renew their nomenclature by using modern and traditional methods. Moreover the observation on the ground underneath the tree provided useful information about the possible tendency to become invasive. The plants were investigated with DNA sequences (ndhF sequences) with a barcoding approach [1], anatomy and terpenes content, redefining the list of the plants and understanding the productivity in essential oils for tropical species of *Melaleuca* cultivated in a mediterranean garden.

Keywords: Artificial intelligence, Digital imaging, Metadata, Specimens

References:

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P35

Euro+Med PlantBase: Documenting plant diversity across Europe and the Mediterranean

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The Euro+Med PlantBase is a comprehensive taxonomic and distributional reference for vascular plants and bryophytes of Europe and the Mediterranean region, including the Caucasus and the Atlantic islands, and one of only four continental-scale plant biodiversity resources worldwide. It integrates knowledge contributed by a community of botanical experts, as well as regional and taxonomic data sources.

The database currently covers approximately 47,000 taxa, comprising 35,000 species and 12,000 subspecies, including about 3,000 non-native taxa, and contains approximately 333,000 distribution records of accepted taxa across 80 countries and other administrative units.

Despite the long history of botanical exploration in the Euro-Mediterranean area, approximately 150–200 species described as new to science are added to the database each year. The data reveal a flora that is notably geographically structured: almost half of the vascular plants recorded in Euro+Med occur in only one administrative unit.

The influence of the Euro+Med PlantBase goes beyond taxonomy and floristics. It has been cited in more than 4,000 scientific publications across many disciplines, currently with 300–400 citations per year, supporting research in plant evolution, ecology, vegetation science, conservation, plant-animal interactions, and biodiversity informatics.

The Euro+Med PlantBase is being launched in an overhauled portal, based on the EDIT Platform for Cybertaxonomy. Its editorial board has been restructured to reflect the diversity of taxonomic expertise across the target region. These changes come in memory of our beloved colleague, the late Eckhard von Raab-Straube, who sadly passed away in 2024, but who was instrumental in curating the database over the past more than two decades.

Keywords: Euro+Med PlantBase, Plant diversity, Biodiversity informatics, Europe and Mediterranean

P36

Towards an online checklist of the vascular plants of Georgia (Caucasus)

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Georgia is a floristically diverse and biogeographically complex country within the Caucasus region. It has a long history of botanical exploration resulting in a substantial body of floristic literature. Nevertheless, taxonomic knowledge is uneven, and many existing floristic works are partly or largely outdated and therefore of limited use for biodiversity research and conservation. We present the concept, scope, and editorial framework for an ongoing work to develop a new, modern, dynamic online checklist of the vascular plants of Georgia. The checklist will be a compilation of available floristic and taxonomic literature and include native and naturalised taxa at family, genus, species and subspecies rank. Particular attention will be given to a conservative treatment of endemics and range-restricted species and the transparent documentation of taxonomic uncertainty. The checklist is intended as a first modern taxonomic baseline rather than a full-scale revision and will be continuously expanded and updated.

Keywords: Vascular plants, Georgia, Online checklist, Taxonomy

P37

An important sand dune area from Northern coastlines of İstanbul, Ağaçlı dunes floristic richness, treats and conservation

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The Ağaçlı Dunes site, situated on the Black Sea coast north of the new İstanbul Airport and west of the Bosphorus, possesses high floristic richness. Over the last 30 years, extensive opencast lignite mining has destroyed thousands of hectares in the region. Today, only small intact patches remain, facing further threats from coastal dune clearing for beach development. Despite severe habitat degradation, the site preserves seven distinct dune vegetation types: early yellow dunes (*Ammophila arenaria*(L.)Link subsp. *arundinacea*(Husn.)H.Lindb. , *Pancratium maritimum* L.), late yellow/early grey dunes (*Centaurea kilaea* Boiss., *Matthiola fruticulosa* (L.)Maire), humid dunes (*Carex colchica* J. Gay, *Juncus acutus* L.), grey dunes (*Alyssum stribrnyi* Velen, *Linum tauricum* subsp. *bosphori* P.H.Davis, *Taeniopetalum obtusifolium* (Sm.)Pimenov, *Teucrium polium* L., *Cistus salviifolius*) L., fixed high dunes (*Isatis arenaria* Azn., *Verbascum degenii* Halacsy), and mixed dune scrub (*Juniperus oxycedrus* L., *Laurus nobilis* L., *Quercus infectoria* Oliv.) [1]. The site harbors globally threatened and endemic species such as *Asperula littoralis* (Sm.) P. Capito & Del, *Centaurea kilaea* Boiss., *Isatis arenaria* Azn., *Linum tauricum* subsp. bosphori P.H. Davis, *Silene sangaria* Coode & Cullen, and *Verbascum degenii* Halácsy, alongside rare taxa including *Artemisia marschalliana* Spreng., *Jurinea kilaea* Azn., *Maresia nana* (DC.) Batt., *Silene dichotoma* Ehrh., and *Stachys maritima* Gouan [2]. This study was conducted within the framework of the "National Biodiversity Inventory and Monitoring Project" of İstanbul, carried out by the General Directorate of Nature Conservation and National Parks (DKMP).

Keywords: Ağaçlı Dunes, Sand dune flora, Endemic species, Conservation, İstanbul biodiversity

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P38

Floristic diversity of the Apiaceae family in Artvin province (Türkiye): An assessment of studies conducted between 2000 and 2026

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Artvin Province is recognized as one of Türkiye's most important centres of plant diversity due to its location within the Caucasus Biodiversity Hotspot, its representation of the Euro-Siberian floristic region, and its direct floristic connection with the Caucasus through Georgia. Hosting approximately 2,727 vascular plant taxa, the province represents a significant centre of genetic diversity, particularly for the Apiaceae (Umbelliferae) family. In Türkiye, Apiaceae is represented by approximately 110 genera and more than 500 species, many of which are characterized by high endemism and considerable ecological and economic importance. In this study, floristic surveys, taxonomic investigations, and herbarium records concerning the Apiaceae family in Artvin Province conducted between 2000 and 2026 were comprehensively evaluated. The results revealed the presence of 51 genera and 109 species belonging to Apiaceae. Among these, seven species are endemic to Türkiye, while 16 taxa are considered rare and of conservation priority. The most species-rich genera were *Peucedanum* and *Pimpinella* (8 species each), followed by *Bupleurum* and *Heracleum* (7 species each), *Chaerophyllum* (6 species), *Anthriscus, Eryngium*, and *Seseli* (5 species each), *Torilis* (4 species), and *Bunium* (3 species). A considerable proportion of the recorded Apiaceae taxa are shared with the Caucasus flora, confirming the role of Artvin as a major biogeographical transition zone between the Anatolian and Caucasian floristic regions. Considering its relatively small geographical area, the occurrence of 109 Apiaceae species represents approximately 22% of the Turkish Apiaceae flora, highlighting Artvin as a national centre of diversity for the family. These findings demonstrate that Artvin is not only a hotspot of floristic diversity but also a priority area for the conservation of endemic and rare Apiaceae taxa. The dataset presented here provides an important baseline for future studies on the taxonomy, biogeography, conservation biology, and sustainable utilization of the Apiaceae family in Türkiye.

Keywords: Artvin, Apiaceae, Caucasus, Flora, Türkiye

References:

[1] Eminağaoğlu, Ö. (Ed.) 2015, Artvin'in Doğal Bitkileri (Native Plants of Artvin), İstanbul: Promat, 456.
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P39

Geophyte taxa naturally distributed in Artvin province, Türkiye

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Artvin Province, located in northeastern Türkiye, is one of the most important floristic regions of the country because of its broad altitudinal range, diverse climatic conditions and rich habitat heterogeneity [1-2]. This study aimed to determine the geophyte taxa naturally distributed in Artvin Province and its districts. Floristic surveys conducted between 1995 and the first half of 2026, herbarium records and relevant literature were evaluated, and the data were supported by specimens deposited in the Artvin Çoruh University Herbarium (ARTH). Taxa were assessed according to family, genus, endemism, IUCN category, phytogeographical region and underground storage-organ type. In total, 205 geophyte taxa belonging to 62 genera and 26 families were identified. Twenty-two taxa were endemic to Türkiye, corresponding to an endemism rate of 10.48%. The richest families were Orchidaceae with 48 taxa (22.86%), Amaryllidaceae with 41 taxa (19.52%) and Asparagaceae with 25 taxa (11.90%). Phytogeographically, 47 taxa (22.93%) belonged to the Irano-Turanian region, 43 taxa (20.98%) to the Euro-Siberian region and 10 taxa (4.88%) to the Mediterranean region, while 105 taxa (51.22%) were widely distributed or of unknown phytogeographical origin. Bulbous geophytes were dominant with 81 taxa (39.51%), followed by tuberous, rhizomatous and cormous geophytes. The results indicate that Artvin is an important geophyte diversity centre in Türkiye and underline the conservation significance of endemic and threatened geophyte taxa.

Keywords: Artvin, Geophytes, Flora, Phytogeography, Endemic plants

References:

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P40

Geographical distribution of *Stachys* Section *Ambleia*

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Stachys L. is one of the largest genera of Lamiaceae, comprising approximately 370 species distributed mainly in temperate and subtropical regions of the Northern Hemisphere. Section *Ambleia* Benth. is a morphologically distinctive lineage characterized by suffruticose perennial habit, dendroid indumentum, xerophytic adaptations, and predominantly 2–6-flowered verticillasters [1]. This section comprises 12 species and 13 taxa worldwide, distributed primarily in the Irano-Turanian and eastern Mediterranean phytogeographical regions. The section includes *Stachys aegyptiaca* Pers., *S. babylonica* Hamodie & Wilcock, *S. cydni* Kotschy ex Gemici & Leblebici, *S. inflata* Benth., *S. kotschyi* Boiss. & Hohen., *S. laxa* Boiss. & Buhse, *S. nivea* Labill., *S. obtusicrena* Boiss., *S. palaestina* L., *S. trinervis* Aitch. & Hemsl., *S. turcomanica* Trautv., and *S. yildirimlii* Dinç, and is distributed across Iraq, Türkiye, Iran, Armenia, Azerbaijan, Lebanon, Georgia, Palestine, Egypt, Syria, the Arabian Peninsula, Turkmenistan, and Afghanistan. Among them, *S. inflata* subsp. *inflata* is the most widely distributed taxon, occurring from the Caucasus through eastern Anatolia and the Zagros Mountains to northern Iraq. In Türkiye, the section is represented by three species, two of which are endemic. *Stachys inflata* occurs in Ağrı (Doğubayazıt), whereas *S. cydni* and *S. yildirimlii* are narrow endemic species restricted to Mersin Province (Arslanköy and surrounding areas). In addition, the geographical distribution pattern of the section, including its northern, southern, eastern, and western range limits, will be evaluated. The distribution boundaries, floristic regions occupied, and species diversity across different countries will be presented to provide a comprehensive overview of the biogeographical characteristics of the section.

Keywords: *Ambleia, Distribution, Stachys*, *Türkiye*

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P41

A new record for the A7 Grid Square in the flora of Türkiye: *Centaurea diffusa* (Asteraceae)

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Centaurea diffusa Lam. (Asteraceae) is a species previously reported in the *Flora of Türkiye* from A1(E), A2(E), A2(A), A4 and B2 grid squares in northwestern and western Anatolia [1]. During floristic field studies carried out in Sera Lake Nature Park and its surroundings in Akçaabat district of Trabzon Province, specimens belonging to the genus *Centaurea* were collected and examined. The material was identified as *C. diffusa* based on its diffusely branched habit, divided leaves, numerous small capitula and characteristic involucral bracts. Comparison of the collection data with the distribution records given in the *Flora of Türkiye* showed that no record had previously been provided for the A7 grid square [1]. The present record therefore represents a new grid-square record for A7 and extends the known distribution of the species to the eastern Black Sea region of Türkiye. The finding also indicates that detailed local floristic surveys remain important for detecting overlooked distributional records, even for taxa already known from other parts of the country. This contribution updates the grid-based distribution of *C. diffusa* and provides additional floristic data for the flora of Trabzon and the Black Sea region.

Keywords: A7 grid square, Asteraceae,*Centaurea diffusa*, New record, Trabzon

References:

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P42

Updated distribution records of *Cynanchum acutum* subsp. *acutum* (Apocynaceae) in Türkiye

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Cynanchum acutum subsp. *acutum* is a perennial climbing taxon native to the Mediterranean Basin and western Asia, and has also been reported as an invasive species in several regions beyond its native range. This study aimed to compile and update the current distribution records of *C. acutum* subsp. *acutum* in Türkiye by integrating published floristic records, herbarium specimens originating from Türkiye and preserved in national and international herbaria, and recent field observations. All occurrence records were verified, georeferenced, and mapped using ArcGIS to produce an updated distribution map and a comprehensive distribution dataset. According to the *Flora of Türkiye*, the taxon had previously been reported from only 26 localities. This study documented 114 additional localities based on literature and herbarium surveys and 15 new localities through fieldwork, increasing the total number of known localities to 155. The updated records reveal that the taxon occurs across a wide range of habitats in Türkiye, including coastal sandy and saline areas, riverbanks, wetlands, roadsides, vineyards, olive groves, abandoned lands, cultivated fields, and open rocky slopes. The resulting dataset provides an updated information on the distribution of the taxon in Türkiye and serves as a valuable reference for future floristic, taxonomic, and biodiversity studies.

Keywords: *Cynanchum acutum* subsp. *acutum*, Distribution map, Türkiye.

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The long-term Pleistocene refugial persistence and continuous interspecific gene flow in the rare tertiary cliff-endemic *Daphne petraea*

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The Southern Limestone Alps are a major centre of Alpine endemism and a key Quaternary refugium during Pleistocene glacial cycles. This region is characterised by an exceptionally buffered mesoclimate, where large peri-Alpine lakes and moderate temperatures generate summer-wet, subtropical-like conditions with comparatively mild, dry, and warm winters. Such long-term environmental stability has enabled the persistence of ancient lineages, including the Tertiary rock-dwelling endemic *Daphne petraea* (Thymelaeaceae), restricted to vertical dolomite cliffs above Lakes Garda, Ledro, and Idro. We tested whether populations on cliffs along the eastern and western shores of Lake Idro constitute distinct phylogeographic lineages with limited recent gene flow. *Daphne petraea* occupies a broad altitudinal range from forest to alpine belts, facilitating secondary contact with two diploid close relatives: the widespread *D. cneorum*, distributed across the European Alps from lowlands to the subalpine zone, and the alpine endemic *D. striata*, typical of rocky alpine grasslands. Population genomic analyses support the presence of two divergent lineages on opposite sides of Lake Idro and reveal multiple homoploid hybridisation events between *D. petraea* and both congeners, mainly in parapatric secondary contact zones. We further quantify shifts in floral morphology in these hybrids and assess their implications for evolutionary trajectories and persistence. Our results indicate that this Tertiary relic is not only part of an "evolutionary museum" but also actively engaged in hybridisation, producing homoploid hybridogenetic offspring. Nonetheless, we detect no pervasive introgression that would threaten *D. petraea* through genetic swamping. Instead, its long-term survival is more likely to be jeopardised by ongoing climate change, associated drought, and increasing habitat hostility, which should be explicitly integrated into risk assessment and conservation planning for this and other relict endemics of the Southern Limestone Alps.

Keywords: Southern Alps, RAD sequencing, Diploid ploidy level

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Türkiye as the centre of plant diversity and evolution explored with the genus *Alyssum* (Brassicaceae): Focus on the European - Anatolian biogeographic connections

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The aim of this research is to elucidate the biogeographic links between Türkiye and Europe and to identify the evolutionary processes that have shaped the plant diversity of these regions, using the genus *Alyssum* (Brassicaceae) as a model system. Owing to its remarkable taxonomic, ecological and cytogenetic diversity, *Alyssum* has proven to be an excellent model for investigating diversification and speciation in Mediterranean and mountain floras. To reconstruct the evolutionary history, biogeographic patterns and diversity of the selected taxa, we will integrate extensive expertise on the study system with a multidisciplinary methodological framework. This approach combines high-throughput next-generation sequencing and advanced bioinformatic analyses with complementary techniques, including multivariate morphometrics, flow cytometry, chromosome counting and ecological niche modelling. The integration of these datasets will enable a comprehensive assessment of genetic, morphological and ecological variation across the studied lineages. The project will contribute to resolving taxonomic relationships within *Alyssum* and provide new insights into the mechanisms underlying the origin and diversification of plant diversity in the Eastern Mediterranean and adjacent European regions. These findings will also offer a robust scientific basis for reassessing patterns of endemism and improving biodiversity conservation strategies in Türkiye and other areas included in the study.

Keywords: Biogeography, Brassicaceae, Hyb-Seq, RADseq, Speciation

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Seed morphology reflects an East–West biogeographic split in Turkish *Campanula* (Campanulaceae)

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Campanula L., comprising approximately 450 species worldwide with a dense distribution in the Northern Hemisphere, is represented in Türkiye by around 150 taxa [1]. Known as "bellflower," the genus exhibits high biological plasticity, so neither traditional morphological studies nor molecular phylogenetic methods alone have been sufficient to resolve its systematic relationships. Although the taxonomic diversity of Campanula in Türkiye has been clearly documented, its systematic relationships have not yet been comprehensively evaluated. Shetler and Morin [2], in their survey of seed morphology in North American Campanulaceae, showed that wing structure can be an important character for distinguishing taxa.

We examined 58 taxa belonging to seven sections: *Symphyandriformes* (Fomin) Charadze, *Rupestres* (Boiss.) Charadze, *Scapiflorae* (Boiss.) Charadze, *Saxicolae* (Boiss.) Charadze, *Tracheliopsis* (Buser) Damboldt, *Dictyocalyx* (Fed.) Damboldt and *Platysperma* Damboldt. At least 20 seeds per population belonging to 83 populations were measured using a stereomicroscope. Quantitative characters used are seed length and width; and qualitative characters included outline, wing structure, wing position, colour, surface ornamentation, three-dimensional shape and degree of compression.

Quantitative and qualitative characters were combined in a Gower distance matrix, which was then subjected to Principal Coordinate Analysis (PCoA) for a taxon-based evaluation. The ordination separated eastern from western taxa along the first PCoA axes, with the two groups overlapping mainly in taxa distributed along the Anatolian Diagonal. Seed morphology, and particularly wing structure, therefore, provides characters congruent with the systematic and biogeographic patterns within Turkish Campanula and offers a useful complement to molecular data.

Keywords: Seed morphology, Seed wing, *Campanula*, Numerical taxonomy, Anatolian Diagonal

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Phylogenetic relationships between Central Asian and Mediterranean species of *Tamarix* (Tamaricaceae)

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The genus *Tamarix* L. (Tamaricaceae) comprises several evolutionary lineages distributed throughout the Mediterranean Basin, the Middle East, Central and East Asia, and southern Africa. Species delimitation within the genus has long been complicated by extensive morphological variation and overlapping diagnostic characters, resulting in persistent taxonomic uncertainty.
Field investigations conducted in the northern part of the Turan region (South Kazakhstan) confirmed the occurrence of 6 *Tamarix* species and revealed considerable morphological variation within several taxonomic complexes. The studied material includes *Tamarix ramosissima* and related taxa, *T. elongata*, *T. hispida*, *T. leptostachya*, and three entities belonging to the *T. laxa* complex. A map with the collection sites for each species is provided.
A preliminary molecular phylogeny based on three plastid regions (trnS–trnG, trnQ–rps16, and ndhF–rpl32) was reconstructed to evaluate the systematic position of the Central Asian taxa. Mediterranean species (*T. gallica, T. africana, T. boveana, T. tetragyna, T. parviflora, T. dalmatica, T. hampeana, T. nilotica,* and *T. aphylla*) were included as phylogenetic reference taxa to provide a broader evolutionary framework for assessing relationships among geographically distinct lineages.
The molecular phylogeny, supported by comparative morphological observations, recovered most Central Asian taxa as a well-supported lineage distinct from the Mediterranean clade. *Tamarix elongata* exhibited morphological similarities to *T. boveana* and *T. tetragyna*, although these affinities were not supported by the phylogenetic reconstruction. Within the *T. laxa* complex, one entity formed a clearly distinct lineage, whereas the remaining two showed only limited genetic differentiation.
These findings improve our understanding of the evolutionary history of *Tamarix* in Central Asia, provide new insights into species boundaries, and establish a foundation for future taxonomic revision and nomenclatural stabilization of the Central Asian representatives of the genus.

Keywords: *Tamarix*, Tamaricaceae, Central Asia, Mediterranean Basin, Molecular phylogeny, Taxonomy, Evolutionary relationships.

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Molecular genetic study of wild-growing apple trees of the Zailiysky Alatau

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Apple forests of Kazakhstan, being the genetic center of origin of the cultivated apple, represent a unique gene pool possessing resistance genes for breeding programs. The range of the relict species *Malus sieversii* (Sievers apple) in the wild encompasses the mountains of the Tian Shan, Pamir-Alay, Kulja (Western China), and Hindu Kush (Northern Afghanistan) [1]; in Kazakhstan, populations of Sievers apple are found in the Western Tian Shan, Tarbagatai, Dzungarian, and Zailiysky Alatau [2]. Molecular genetic studies of the relict species Malus sieversii are of particular importance in the context of active infrastructural development of mountain territories.

The aim of the study is to differentiate natural populations of *Malus sieversii* and hybrid forms arising from possible introgression with cultivated and introduced representatives of the genus Malus in the Butakovka and Kimasar gorges.

The ISSR method was applied to identify genetically distinct groups and to detect specimens with signs of possible hybrid origin without prior knowledge of the genome sequence. Genetic similarity indices were calculated between specimens, on the basis of which cluster analysis was performed using the UPGMA method.

The results of the cluster analysis revealed the division of the studied specimens into two main genetic clusters, indicating pronounced genetic differentiation within the studied populations of Sievers apple.

Based on the cluster analysis using ISSR markers and the UPGMA dendrogram construction method, the control cultivar 'Golden Delicious' (alma) did not form a separate isolated branch, but instead grouped within the same cluster as a number of studied specimens presumed to represent hybrid forms. This distribution indicates genetic similarity between a portion of the studied specimens and the cultivated apple, which may suggest processes of interspecific hybridization and probable introgression of *Malus domestica* genetic material into natural populations.

At the same time, specimens identified as typical forms of *Malus sieversii* formed a separate cluster characterized by relative genetic distinctiveness. The obtained results indicate the heterogeneity of the genetic structure of natural populations and the presence of areas with signs of potential genetic admixture.

The identified patterns are of significant conservation importance, as they confirm the risk of disruption to the genetic integrity of *Malus sieversii* populations growing in the Butakovka and Kimasar gorge areas under conditions of anthropogenically transformed landscapes. This substantiates the need to identify and preserve genetically authentic populations as objects of special protection and to restrict economic and infrastructural activities in the respective territories.

Keywords: *Malus sieversii*, ISSR-PCR, Genetic similarity, Interspecific hybridization

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A chromosome-scale reference genome for wild cardoon reveals signatures of globe artichoke domestication

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The wild cardoon (*Cynara cardunculus* var. *sylvestris*) is the closest wild relative and progenitor of the globe artichoke (*C. cardunculus* var. *scolymus*), but its genomic features and role in artichoke domestication remain incompletely understood. Here, we generated a chromosome-scale genome assembly of the wild cardoon, providing a high-quality reference for investigating genome evolution and domestication in *C. cardunculus*. For comparison, we also assembled the genome of globe artichoke cv. "Brindisino". Both assemblies showed high contiguity (N50 >56 Mb) and completeness (>97% BUSCO). Genome-wide synteny revealed extensive conservation of chromosome structure despite substantial structural variation, while divergent regions of the cultivated genome were enriched in genes involved in vesicle trafficking and sesquiterpene biosynthesis. Resequencing of artichokes, cultivated cardoons, and wild cardoons identified more than 6 million high-confidence SNPs and revealed markedly higher heterozygosity in clonally propagated artichokes. Population analyses separated artichokes from cardoons and identified distinct genetic groups within cultivated germplasm. Comparison with the wild cardoon genome revealed regions fixed in artichoke containing candidate genes associated with flowering, reproductive development, stress responses, and phenylpropanoid metabolism, indicating localized signatures of domestication. High-impact variants further highlighted divergence in developmental, signaling, and defense-related pathways, while gene family analyses showed expansion of functions related to specialized metabolism, hormone biosynthesis, and defense in artichoke. Overall, the wild cardoon genome provides a valuable reference for understanding the evolution and domestication of *C. cardunculus*, supporting future studies of genetic diversity and genomics-assisted breeding.

Keywords: *Cynara cardunculus* genome, Wild cardoon, Globe artichoke, Domestication signature, Vegetative propagation, Flowering and reproductive genes, Resistance genes

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The Importance of *in silico* genomic approaches in plant taxonomy and phylogeny: An agronomic perspective

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Traditional morphology-based plant taxonomy can be constrained by phenotypic plasticity, convergent evolution, hybridization, and polyploidy, which may obscure species boundaries and evolutionary relationships. The rapid expansion of high-throughput sequencing and in silico phylogenomic approaches has therefore transformed plant systematics by enabling the simultaneous analysis of nuclear, plastid, mitochondrial, and transcriptomic data across large taxon sets [1]. Genome skimming, target enrichment, Hyb-Seq, de novo assembly, orthology inference, and model-based phylogenetic analyses can increase resolution among closely related or taxonomically problematic groups, reveal reticulate evolutionary histories, and support more robust taxonomic revisions. These approaches are also increasingly important from an agronomic perspective because genomic characterization of crop wild relatives can identify alleles and structural variants that were lost or reduced during domestication and modern breeding. Türkiye is particularly relevant in this context because its position at the intersection of the Mediterranean, Irano-Turanian, and Euro-Siberian phytogeographical regions supports high plant diversity, numerous endemic taxa, and important wild relatives of cultivated species. Genomic studies of wild *Cicer* populations from southeastern Anatolia, for example, have demonstrated substantial untapped diversity with potential value for improving cultivated chickpea and increasing resilience to heat, drought, and other stresses [2]. Similar in silico strategies can be extended to wheat progenitors, legumes, sunflower relatives, and economically important grasses to characterize gene pools, prioritize germplasm conservation, and guide pre-breeding. Integrating phylogenomics and population genomics with classical taxonomy and field-based characterization can thus connect evolutionary knowledge with practical crop improvement. This comprehensive framework, while supporting climate-change-resilient breeding, sustainable agriculture, and evidence-based management of plant biodiversity, is particularly valuable for conserving Türkiye's genetic resources.

Keywords: Plant phylogenomics, Plant taxonomy, Crop wild relatives, Genetic resources, Genomic breeding

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P50

Railway transport as a pathway for the introduction and spread of alien species into the Bulgarian flora

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Railway transport is widely recognized as one of the significant pathways for the introduction and spread of alien plant species worldwide. The railway network and train compositions fall into two main pathways for the introduction of alien species, according to the CBD classification – "Transport – Contaminant", which is carried out through trade of contaminated commodities, and "Transport – Stowaway", which is realized by accidental attachment of plant propagules to train compositions, as well as by accidental transfer of viable plant parts (mainly seeds) through passenger traffic. Dozens of alien species from the alien flora of Bulgaria are closely associated with the railway network. For example, over 20% of all alien species reported as new to the flora of Bulgaria after 2000 are associated with the railway network. Some alien species, the distribution of which is common on the railway network are *Ambrosia artemisiifolia*, *Bidens bipinnatus*, *Erigeron canadensis*, *E. sumatrensis*, *Euphorbia davidii*, *E. maculata*, *E. prostrata*, *Grindelia squarrosa*, *Lepidium virginicum*, *Senecio inaequidens*, etc. Of the species listed under the Regulation (EU) No 1143/2014, *Ailanthus altissima* is commonly found on the railway network. The poster presents the diversity of the alien plant species on the railway network in Bulgaria, as well as some taxa newly recorded for the flora of the country.

Keywords: Alien plants, Bulgarian flora, Invasive alien species, Railroads

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The paradox of biological invasions: *Agave* and *Opuntia* as cultural and symbolic elements in the European Mediterranean

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The European colonization of the Americas facilitated the introduction into Europe of a large number of plant species native to the American continent (the "Columbian Exchange"). Several of these species rapidly gained economic importance, particularly for food production (e.g., *Solanum lycopersicum* and *Theobroma cacao*) and medicinal use (e.g., species of the genus *Cinchona*). Other species were introduced for ornamental or industrial purposes, including several species of the genera *Agave* and *Opuntia*. Plants of these to latter genera reached the Mediterranean region during the sixteenth century and, within a relatively short period, became remarkably integrated into the landscape through both extensive cultivation and naturalization. In some areas, the expansion of *Agave* and *Opuntia* was so extensive that they eventually became highly invasive, posing a serious threat to local biodiversity. In response, management programmes have been developed to control or eradicate these species. However, such initiatives often encounter considerable social resistance. In recent years, movements advocating the "protection" of these plants against control and eradication measures have emerged, as *Agave* and *Opuntia* are widely perceived as characteristic elements of the local landscape and, in many cases, as part of the cultural identity of the regions where they occur. Unfortunately, the contemporary use of these species—as tourist attractions (for example, in Sicily, where ceramics depicting *Opuntia*, a true symbol of the island, are among the most common souvenirs) or even as icons of nature conservation—is becoming increasingly widespread. These perceptions and uses often conflict with the objectives and actions of biodiversity conservation and invasive species management.

Keywords: *Agave*, Iconic species, Naturalization, *Opuntia*, Uses.

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Plant Smartly! A practical tool to prevent the spread of invasive alien plant species in Northeastern Iberian Peninsula

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"Plant Smartly!" is a practical, science-based guide aimed at preventing the spread of invasive alien plant species that threaten local biodiversity, particularly endangered flora and habitats of community interest (i.e., those protected under the European Union Habitats Directive) in the northeastern Iberian Peninsula. It takes the form of a catalogue offering safe plant alternatives to invasive and potentially invasive ornamental species currently available on the market. The guide was developed through collaboration with the ornamental plant sector and supports the *Code of Conduct: Avoiding the Trade and Use of Invasive Alien Plants* produced within the LIFE medCLIFFS project (LIFE20 NAT/ES/001223). This project focuses on improving the management of invasive alien plants threatening Mediterranean cliffs that host endemic *Limonium* species (HCI 1240). The catalogue prioritizes native plant species, which are already adapted to local climatic conditions and therefore most suitable for use in the region. It also includes selected non-native species assessed as posing no invasion risk, as well as safe sterile cultivars. By providing a broad set of locally available alternatives, the guide helps replace problematic species while maintaining diversity in flower colour, growth form, and tolerance to sun and shade conditions. "Plant Smartly!" is intended as a valuable resource for all stakeholders in the ornamental plant sector, including producers, distributors, and both private and public customers. By integrating ecological responsibility with horticultural design and market needs, it promotes informed decision-making without compromising aesthetic value or economic viability. While the standalone catalogue serves as a useful tool, surveys have also been conducted during the project to assess its impact and effectiveness. Based on insights gathered prior to implementation, a shift in public perception is expected by the end of the project.

Keywords: Alien flora, Alternatives, Invasive alien species, Native flora, Mediterranean cliffs.

P53

The Cactaceae family in Sardinia: Distribution, invasion dynamics and control measures

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The introduction of alien species is among the most widespread negative results of human activities. These impacts are particularly severe on islands, which are highly vulnerable to biological invasions due to their ecological isolation, high levels of endemism and increasing anthropogenic pressures associated with tourism [1].

Sardinia is the second largest island in the Mediterranean Sea, located in the central-western part of the basin. Since the 18th century, human activities have promoted the spread of Cacti in Sardinia, widely cultivated for food production, hedging, and ornamental purposes. Cacti success on island is mainly due to strong tolerance to aridity and high temperatures, making them particularly adapted to different habitats, especially in the context of predicted climate change. Moreover, their efficient vegetative reproduction, along with their ability to reproduce by seed and even tolerate salt stress during germination, further supports their establishment and spread in Mediterranean environments, including coastal areas [2].

This study aims to evaluate the current Cactaceae distribution in Sardinia and to analyze the distribution patterns and the environmental factors driving their occurrence and expansion.

Cactaceae occurrence data were collected through a review of published literature, herbarium collections, and field surveys conducted across Sardinia and its surrounding islands in the last 25 years. All records were processed using cartographic and GIS software (QGIS) to analyse their occurrence both close and far from human settlements, within protected areas, their associated habitat types, and environmental conditions. Distribution analyses enabled the identification of the most abundant and widespread Cactaceae taxa in Sardinia, providing a robust basis for prioritizing control and eradication actions. In addition, these data will support the development of species distribution models and predictive maps under future climate scenarios, helping to identify areas potentially vulnerable to cactus invasions, and providing valuable information for early detection and prevention strategies.

Keywords: Alien vascular flora, Cacti, Invasive plants, Mediterranean Basin, *Opuntia*.

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P54

Threatened flora of temporary aquatic habitats of the Parc Natural de Cap de Creus (NE Catalonia, Spain): Results of the 2025 censuses

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Assessing the conservation status of plant taxa associated with temporary aquatic habitats presents particular challenges due to the changing conditions to which they are subject, resulting in drastic fluctuations in their populations. In 2021 and 2022, censuses of *Isoetes durieui* (a semi-aquatic lycophyte of Mediterranean meadows temporarily flooded in spring) and *Spiranthes aestivalis* (an orchid of peat bogs, lagoons, and wet meadows) were carried out in the Cap de Creus Natural Park (PNCC), located in NE Catalonia, Spain. Both species are associated with dry riverbeds and temporary lagoons and were listed as "vulnerable" in the Catalogue of Threatened Flora of Catalonia until 2023 (when the latter was removed from the list). In 2025, due to the high rainfall recorded, the status of the populations was reassessed under optimal conditions for their growth (given that in 2022, the year of the last monitoring, rainfall was very scarce).

In the case of *Isoetes durieui*, 10,125 individuals were counted in 2025, representing a drastic increase of 7,500% compared to previous censuses. Five populations with historical records were rediscovered, and a new population was located. As for *Spiranthes aestivalis*, 353 individuals were counted, representing an 830% increase compared to the previous census. Furthermore, a previously reported population was rediscovered, and a new population was located. These results reflect an apparently favorable situation for both species. However, the fragility of temporary habitats and the pressure from external threats require periodic monitoring. During the 2025 census, for example, signs of eutrophication and soil poaching and compaction were detected in historical locations, along with an increasing presence of invasive species (mainly *Arundo donax*, *Cyperus eragrostis*, and *Opuntia stricta*). Therefore, regular monitoring should be accompanied by strengthened invasive species control and management, and awareness campaigns targeting land users.

Keywords: Threatened flora, Cap de Creus, Temporary aquatic habitats, Censuses; Conservation

P55

Bulgaria's high mountain flora at risk from climate change

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The high-mountain flora of Bulgaria is represented by species adapted to the harsh conditions of the alpine and subalpine belts (above 1500–1800 m above sea level) – low temperatures, thick snow cover, strong winds, physiological drought and intense solar radiation. In conditions of rapid climate change, these plant species are at risk, as alpine ecosystems are highly sensitive to global warming.
The present study aims to identify the most vulnerable to climate change representatives of the Bulgarian flora in order to provide scientific support for their conservation.
The study was conducted in the period 2018-2025 and included field research in the high mountains of Bulgaria, as well as an analysis of the available literature. The largest number of target species were identified in the following floristic regions: Rila Mts, Pirin Mts, Stara Planina (Central), Vitosha Mt., and the Rhodopes (Western). The richest in species and genera are the families Asteraceae, Rosaceae, Poaceae, Caryophyllaceae, Scrophulariaceae, and Fabaceae. The presence of endemic taxa and taxa of conservation concern, is remarkable. Special attention is paid to species whose only or very few occurrences in the country are found in high mountain environments. The study highlights the key significance of the high-mountain flora in plant diversity conservation and delivers a reliable database for improving management strategies within the country.

Keywords: Bulgaria, High-mountain flora, Plant conservation, Taxonomic analysis

NOT PRESENTED

P56

IUCN Red list assessment of the endemic species *Tanacetum erzincanense* (Asteraceae)

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Tanacetum erzincanense Korkmaz, Kandemir & İlhan was first described from Erzincan, eastern Türkiye, in 2015 [1]. In this study, current distribution, population status, threats, and conservation requirements were re-evaluated in accordance with the IUCN Red List Categories and Criteria [2].
As a result of field surveys conducted in 2024 and 2025, in addition to the population at the type locality in the Mercan district of Erzincan Province, three additional geographically isolated localities were identified in the northern and northwestern parts of Tercan district. *T. erzincanense* is represented by three subpopulations distributed across four localities, with the total number of mature individuals estimated at approximately 18,000–19,000. The largest subpopulation comprises approximately 17,000–18,000 mature individuals and accounts for more than 90% of the total mature population. The other two subpopulations are relatively very small. Therefore, the populations were assessed as not being severely fragmented. The extent of occurrence (EOO) was calculated as 70 km², while the area of occupancy (AOO) was 12 km². The currently known subpopulations are confined to steppe habitat fragments embedded within agricultural fields. The major threats affecting each subpopulation include habitat conversion to agricultural land, nomadic grazing activities, renewable energy investments, and drought events associated with climate change. Considering the geographic distances among the subpopulations and the likelihood that threats affect each subpopulation through distinct dynamics, the number was estimated at 3. A continuing decline in habitat quality and population size was inferred.
Due to its restricted distribution, low number of locations, and ongoing habitat loss, *T. erzincanense* has been assessed as EN (Endangered) according to IUCN categories and criteria [(B1ab(ii, iii,v)+2ab(ii,iii,v)]. There are currently no conservation efforts in place for this species. To ensure its long-term survival, its habitats should be brought under legal protection, site-based management plans should be developed, its seeds should be conserved in gene banks, and local-level awareness-raising should be enhanced. This study contributes to the identification of priority areas for conserving Türkiye's endemic plant diversity.

Keywords: *Tanacetum erzincanense*, Endemic, IUCN, Erzincan, Conservation biology.

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P57

Conservation of *Acer monspessulanum* subsp. *ibericum* - Studies of the species distribution and seed storage behaviour at the National Botanical Garden of Georgia

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Acer monspessulanum subsp. *ibericum* (M.Bieb. ex Willd.) Yalt. (target species) (Georgian maple, Caucasian maple), distributed in Iran, North Caucasus, Transcaucasus, Türkiye, represents the eastern Caucasian-Anatolian geographical race of the Mediterranean species complex of *Acer monspessulanum* L. [1, 2].

IUCN Red list assesses *Acer monspessulanum* L. as LC [3], but its eastern Caucasian-Anatolian taxon, formerly known as *Acer ibericum* M. Bieb. ex Willd., is included in the Red List of Georgia with Vulnerable (VU) status [4]. It is a characteristic species of open arid woodlands, occurring mainly as scattered individuals in the south-eastern part of the country, including Dedoplistskaro and Bolnisi municipalities, Shida Kartli and the surroundings of Tbilisi [4].

During 2018–2019 a notable population dominated by the target species, located on steep eastern-facing slopes near Betania Monastery, close to Tbilisi was studied in detail. Part of this population was affected by the flood and landslide in the gorge of river Vere in 2015. Other natural populations are represented by isolated trees or small groups. Human activities, including the construction of BP's Western Route Export Pipeline, resulted in the loss of numerous individuals in the Kvemo Kartli population, located in the Khrami River gorge near the pipeline.

In the Seed Bank, operating at the National Botanical Garden of Georgia, are preserved several documented seed collections of the target species, collected through the Millennium Seed Bank Partnership (MSBP), including samples from Dedoplistskaro district, Vashlovani National Park, Mt. Shavi Mta, (2006, 2015) and Betania, Tbilisi Adminisrative area (2019). These collections, along with distribution maps and habitat data provide an important basis for developing conservation strategies and assessment of the conservation status.

Seeds of the target species are classified as orthodox [6]. Although studies are available on seed longevity and storage conditions for various species within this genus, experimental data specifically addressing the long-term storage of *Acer ibericum* seeds at low temperatures are currently lacking. Viability of seeds, collected in 2015, processed according to the MSBP standards and stored at -20°C in the seed bank of NBGG with a relative humidity, reduced to 13-12%, was tested using the tetrazolium (TZ) staining method, as according to international protocols, seeds stored for the long-term are re-tested every 10 years [6,7].

Testing of viability of randomly chosen seeds by TZ method [7] showed positive results: the fully developed embryo remained viable, with all parts stained in red. However, morphological prove of the viability does not confirm germination capacity. As species of this genus have deep physiological dormancy, seeds require a prolonged germination period after the application of dormancy-breaking treatments. Germination testing is currently ongoing to further assess viability of all seed collections.

Living collections with up to 15 cultivated individuals have been maintained at the National Botanical Garden of Georgia (NBGG) since 1902.

Keywords: Red List, Conservation status, Habitat, Ex situ conservation, Seed viability.

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Population genomic analysis of the endemic *Rhaponticoides iconiensis* Using ddRAD-Sequencing

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Rhaponticoides iconiensis (Hub.-Mor.) M.V.Agab. & Greuter is a species known from only a few populations in Türkiye and is listed as Critically Endangered on the IUCN Red List. In this study, 26 individuals from two populations (Konya and Karaman) were collected and the genetic diversity and population structure of the species were examined using ddRAD-seq (double digestion restriction site-associated DNA sequencing). A total of 44559 high-quality SNPs were detected with ddRAD-seq. Genetic diversity was found to be higher in the Konya population (Hs: 0.48194) than in the Karaman population (Hs: 0.17116) among the populations belonging to the species. Moreover, high genetic differentiation (Fst: 0.5436) was detected between the populations. ddRAD-seq-based population genomic analyses offer an effective approach for rapidly and reliably assessing the conservation status and threat levels of endemic species with limited distribution through high-resolution genomic data.

Keywords: Asteraceae, Endemic, Genetic diversity, Population genetics, Türkiye

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P59

Ecophysiology of seed germination of *Bituminaria bituminosa* and *B. morisiana* in response to scarification and thermal shock

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Mediterranean Fabaceae play a fundamental ecological role in natural ecosystems and represent valuable resources for biodiversity conservation, valorisation for forage uses and ecological restoration [1]. Within this family, two perennial species are *Bituminaria bituminosa* (L.) C.H.Stirt. distributed throughout the Mediterranean Basin and *B. morisiana* (Pignatti & Metlesics) Greuter a Sardinian endemic species mainly associated with rocky habitats. Understanding seed dormancy and germination ecophysiology is essential for *ex situ* conservation and the development of effective propagation protocols. This study investigated the germination responses and dormancy breaking requirements of both species using fresh seeds and seed lots stored at the germplasm bank. Germination tests were conducted on nine accession and included control, mechanical scarification, and heat shock treatment. Control tests showed generally low germination percentages, remaining below 30% in most accessions, although two populations of *B. morisiana* reached values around 60%. Mechanically scarified seeds consistently achieved high germination percentages (>90%) regardless of species, accession, or incubation temperature. Scarification also resulted in higher germination speed, with 50% germination achieved within six days. Heat shock treatment produced more variable responses among populations. In *B. bituminosa*, exposure to 80°C for five minutes significantly improved germination, with final germination percentages between 50% and 80%. In *B. morisiana*, responses were more heterogeneous, with some populations showing germination values comparable to controls and others showing a high germination percentage. Seed viability was largely maintained after heat treatment, indicating considerable thermal tolerance and suggesting an adaptive trait in Mediterranean habitats affected by recurrent fires. Overall, the results support the presence of physical dormancy in both species, associated with a water-impermeable seed coat, and identify mechanical scarification as an effective treatment for breaking dormancy for conservation and propagation purposes. These findings provide useful insights for germplasm management and the restoration programs of Mediterranean plant communities.

Keywords: Germination, Seed, dormancy, *Bituminaria*, *Ex situ* conservation

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P60

Seed microbial biopriming promotes plant establishment in Mediterranean coastal wetlands: Nature-based solutions for ecological restoration

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Mediterranean coastal wetlands are among the ecosystems most threatened by climate change [1], where increasing salinization is expected to compromise plant recruitment, reduce biodiversity, and ecosystem resilience. Developing restoration strategies that enhance the establishment of native species has therefore become a priority. Nature-based Solutions (NbS) based on native represent a promising approach for enhancing plant adaptation to environmental stress [2].

This study evaluated the potential of seed biopriming with microorganisms isolated from native biological soil crusts to improve germination and plant establishment of three characteristic coastal wetland species: Arthrocaulon meridionale, Juncus acutus, and Mentha aquatica. Seeds were inoculated with either a consortium of native plant growth-promoting bacteria or a native cyanobacterial strain and exposed to increasing salinity (0, 0.3, 0.5 and 0.7 M NaCl). Germination percentage and root development were assessed.

Salinity negatively affected seed germination in all species, although species differed in their salt tolerance. Seed biopriming mitigated these effects by improving germination and early root development. In Arthrocaulon meridionale, cyanobacterial inoculation increased germination by 7% over the control at 0.5 M NaCl and was the only treatment supporting both germination and root development at 0.7 M. In Juncus acutus, bacterial inoculation increased germination from 2% in untreated seeds to 8% at 0.3 M NaCl, while cyanobacteria increased it to 6%; however, only cyanobacteria sustained germination (2%) and seedling development at 0.7 M. Germination in Mentha aquatica was completely inhibited under saline conditions, whereas under non-saline conditions cyanobacterial and bacterial inoculation increased germination by 15% and 4%, respectively, compared with controls. Microbial inoculation also promoted root development across all species, with cyanobacterial treatments consistently producing the longest roots.

Our findings highlight the potential of native soil microbiota to enhance Mediterranean coastal plant establishment under increasing salinity, providing an innovative NbS for restoration ecology in climate-threatened Mediterranean coastal wetlands.

Keywords: Salinity stress, Microbial inoculants, Cyanobacteria, Biological soil crusts, Seed germination

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P61

A new significant monumental plant in Sicily: The ancient bitter almond tree (*Prunus amygdalus* var. *amara*) from Castronovo di Sicilia, Sicani Mountains (Italy)

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Sicily preserves an outstanding heritage of monumental trees documented through several regional surveys carried out over the last decades. Previous studies recorded only a few monumental almond trees (*Prunus amygdalus* Batsch) in the Sicani Mountains and elsewhere in Sicily, all exhibiting trunk circumferences only slightly exceeding 3.3 m [1, 2, 3]. According to the international Monumental Trees database [4], 39 living monumental almond trees are recorded from seven countries (Bulgaria, France, Germany, Italy, Morocco, Spain and Türkiye). Among these, the largest documented specimens are located in Rosolini (Sicily, Italy) and Chassagne (France): 4.45 and 4.39 m trunk circumference respectively.

During recent botanical field surveys in the Sicani Mountains (central-western Sicily, Italy), completed in May 2026, an exceptional monumental bitter almond tree was discovered on the eastern slope of Contrada Santa Caterina, near the locality Il Cassaro, in the countryside of Castronovo di Sicilia (37.693322° N, 13.593184° E; 910 m a.s.l.) [4]. The tree grows on calcareous substrate in an abandoned agricultural landscape and is currently not subject to any formal conservation measures. The specimen exhibits a regular spiral trunk that divides into three primary scaffold branches. The trunk circumference measured on the undivided stem immediately below the first branching is 4.60 m, while the girth measured at breast height (1.30 m above ground) reaches 5.20 m. The tree is approximately 9–10 m tall, with a crown spread of 16–18 m and a preliminary age estimate exceeding 500 years. Despite its apparent abandonment, the tree is in excellent phytosanitary condition. The fruits are large (approximately 4 × 3 × 1.5 cm), with a hard shell enclosing a single, consistently bitter kernel (approximately 3 × 1.5 × 0.5 cm). This combination of traits suggests a possible historical use in traditional local confectionery.

Based on the currently available international inventories, the Castronovo di Sicilia almond tree represents the largest documented living monumental almond tree recorded in the Monumental Trees database [5] and, to the best of our knowledge, the largest living almond tree currently documented worldwide. Beyond its exceptional size and longevity, this discovery highlights the importance of integrating field botany, historical evidence, and traditional ecological knowledge for the conservation of Mediterranean plant genetic resources, providing a valuable basis for future dendrometric, genetic, and pomological investigations. Furthermore, the occurrence of consistently bitter kernels indicates that this specimen belongs to the traditional bitter almond group, historically referred to as *Prunus amygdalus* var. *amara* (Duhamel) Focke. To the best of our knowledge, this represents the first documented case of monumentality reported for this traditional botanical variety.

Keywords: *Prunus amygdalus* var. *amara, Monumental trees, Agrobiodiversity, Plant genetic resources, Sicily*.

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Integrating ex-situ and in-situ conservation for endemic plant diversity in the central Anatolian steppe: A case study from Ankara, Türkiye

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The Central Anatolian steppe is one of the richest centers of plant diversity and endemism within the Irano-Turanian phytogeographical region, but its flora is increasingly threatened by urbanization, industrial development, habitat destruction, and climate change. To support the long-term conservation of this unique biodiversity, we established the first integrated in-situ and ex-situ plant conservation area in Türkiye within the Kazan Soda license area (Ankara). Floristic surveys recorded 258 vascular plant taxa, including 41 endemic species. A species-rich marl-steppe habitat (5,360 m²) was designated as a protected area, where naturally occurring vegetation was conserved while threatened species from nearby populations were translocated. In total, 185 plant taxa belonging to 43 families, including 29 endemic species, are currently protected. Seeds of six priority endemic taxa were collected and deposited in the National Seed Bank of Türkiye to secure their genetic diversity. Monitoring of translocated populations demonstrated successful establishment and high survival of nearly all species. In addition to habitat and species conservation, the project promotes public awareness through educational activities, a visitor center, and interpretive displays. This study demonstrates that integrating habitat protection, species translocation, seed banking, and environmental education provides an effective and practical conservation model for safeguarding endemic steppe flora and can serve as a framework for biodiversity conservation in other threatened ecosystems of Türkiye and the Irano-Turanian region [1].

Keywords: Biodiversity, Central Anatolia, Conservation, Flora, Steppe

[1] Duman, H. et al., *Ecologies* 2024, 4, 664-678.

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The role of botanical gardens in the conservation, sustainable cultivation, and value-added product development of medicinal and aromatic Plants: The Ali Nihat Gökyiğit Botanical Garden model

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Artvin Province is one of the richest regions in Türkiye in terms of plant diversity, harbouring approximately 2,727 vascular plant taxa, including nearly 850 medicinal and aromatic plant (MAP) species. However, increasing demand for MAPs, uncontrolled harvesting, habitat degradation, and climate change threaten these valuable plant genetic resources. To address these challenges, Artvin Çoruh University has developed an integrated model within the framework of the Regional Development-Oriented Specialization Programme, combining the conservation, cultivation, research, and value-added utilization of medicinal and aromatic plants. Established in 2018, the Ali Nihat Gökyiğit Botanical Garden (ANGBB), one of the 13 botanical gardens in Türkiye affiliated with Botanic Gardens Conservation International (BGCI), serves as the core implementation centre of this model. The garden maintains living and seed collections, conducts floristic surveys, DNA barcoding, and in vitro propagation studies, and provides demonstration gardens and educational activities. A 700 m² research and exhibition greenhouse, a 500 m² production greenhouse, and model cultivation areas support plant domestication, sustainable cultivation practices, and farmer training, thereby reducing harvesting pressure on natural populations. A key component of the model is the Plant Processing and Product Development Center. Equipped with distillation, extraction, evaporation, spray-drying, and freeze-drying technologies, the center converts cultivated MAPs into essential oils, hydrolates, standardized extracts, and other high-value products. A newly established 1,000 m² fruit processing and storage facility further supports the production of jams, marmalades, fruit purées, and aseptically filled fruit juices. Supported by the Presidency of Strategy and Budget, the Ali Nihat Gökyiğit Foundation, and the European Union Interreg VI-B NEXT Black Sea Basin Programme, this integrated model demonstrates how botanical gardens can simultaneously conserve biodiversity, support scientific research, promote sustainable cultivation, facilitate technology transfer, and contribute to regional development.

Keywords: Artvin, Medicinal and Aromatic Plants, Botanical Garden, Value-Added Products, Türkiye

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Mediterranean university campuses as living laboratories for urban nature restoration under the EU Nature Restoration Regulation

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The entry into force of the EU Nature Restoration Regulation (Regulation (EU) 2024/1991) [1] has established ambitious targets for restoring urban ecosystems, recognizing urban green infrastructure and tree cover as essential components for biodiversity conservation, climate resilience and human well-being. In particular, Article 8 highlights the need to halt the loss of urban green spaces and tree canopy cover while promoting their long-term enhancement. Within this framework, Mediterranean university campuses represent valuable living laboratories where restoration strategies can be assessed through science-based approaches. This work presents the University of Alicante campus as a case study to evaluate the role of university tree collections in supporting urban nature restoration. The study is based on the development of a comprehensive taxonomic inventory of the campus trees, including species identification, georeferencing, photographic documentation and the preparation of identification tools. These data provide a robust baseline for assessing tree diversity, taxonomic composition, the representation of Mediterranean and non-Mediterranean woody species, and the potential contribution of urban tree systems to biodiversity conservation. Beyond the generation of botanical inventory, this initiative proposes a methodological framework for integrating taxonomic knowledge into the assessment and sustainable management of urban green infrastructure. The resulting information will facilitate future analyses related to ecological resilience, species diversity, ecosystem services and climate adaptation, providing scientific evidence that may support restoration planning in Mediterranean urban environments. University campuses combine scientific knowledge, long-term management and high plant diversity, making them ideal platforms for testing restoration-oriented approaches that can later be transferred to other urban settings. The proposed framework contributes to the implementation of the EU Nature Restoration Regulation by demonstrating how taxonomic inventories can support biodiversity assessment and evidence-based decision-making for the restoration of Mediterranean urban ecosystems.

Keywords: Urban Nature Restoration; Urban Trees; Mediterranean Biodiversity; Regulation (EU) 2024/1991.

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P65

Microplastics in honey: Ecological transport mechanisms, bioindication, and impacts on honeybee gut microbiota

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In recent years, the global proliferation and systemic infiltration of microplastics (MPs) into biological systems have necessitated a detailed investigation into the extent of contamination and potential ecotoxicological impacts on honey products. Indeed, honey undergoes a complex process shaped within the mouthparts and honey crop of bees, involving numerous botanical and ecological factors from raw material collection to in-hive maturation. This endows honeybees with a central role in determining the chemical and biological structure of honey. During flight, honeybees accumulate electrostatic charges that effectively capture atmospheric or environmental microplastics, subsequently transporting them to the hive during nectar and pollen foraging. This ecological transport mechanism renders honey and its pollen spectrum sensitive environmental bioindicators reflecting regional contamination levels. On the other hand, a substantial proportion of microplastics detected in honey directly originates from honey extraction, processing equipment, and packaging procedures [1]. Exposure to these polymer structures—introduced through both environmental and industrial pathways—induces gut dysbiosis by reducing beneficial bacteria in the bee gut, triggers biofilm formation in tissues, and impairs nutrient absorption. Furthermore, microplastic accumulation restricts the ability of honeybees to detoxify pesticides, leaving them vulnerable to pathogens [2]. This study comprehensively addresses the value of honey as an environmental pollution bioindicator, the relationship between pollen profiles and regional contamination, the predominant polymer profiles encountered in honey, the destructive effects of these polymers on honeybee health and gut microbiota, as well as novel methodological approaches aimed at investigating this emerging issue.

Keywords: Microplastics, Honey, Pollen, Bioindicator, Bee gut microbiota

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Antibacterial and synergistic activity of *Padina pavonica* collected from Northern Cyprus in combination with Ciprofloxacin

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The ongoing antimicrobial resistance crisis highlights the importance of novel antimicrobial agents. Understudied bioactive compounds from marine natural products offer new options for antimicrobial agents against pathogenic microorganisms [1]. The purpose of this study was to assess antibacterial and synergistic activities with ciprofloxacin of a brown seaweed, *Padina pavonica*, against *Escherichia coli* ATCC 25922, *Klebsiella pneumoniae* ATCC 700603, *Enterococcus faecalis* ATCC 29212, and *Staphylococcus aureus* ATCC 25923 *via* broth microdilution method as described in CLSI [2]. Two different extraction methods, maceration using methanol (MA); and fractionation, in increasing polarity, using hexane (HF), ethyl acetate (EAF) and methanol (MF), were utilized to obtain bioactive compounds and compare their extraction efficiencies. All of the extracts exhibited promising antibacterial activity against *E. faecalis*; however, no inhibitory activity was detected against any of the other bacterial strains tested. The antibacterial assay revealed significant minimum inhibitory concentration (MIC) values of 0.125 ± 0.02 mg/mL, 0.25 ± 0.04 mg/mL, 0.5 ± 0.17 mg/mL, and 0.25 ± 0.08 mg/mL against *E. faecalis* for HF, EAF, MF, and MA, respectively. Moreover, to evaluate the synergistic activity of *P. pavonica* in combination with ciprofloxacin against *E. faecalis*, a fractional inhibitory concentration (FIC) index assay was utilized. The binary combinations of ciprofloxacin and seaweed extracts did not reveal any antagonistic activity. All binary combinations increased the activity of either ciprofloxacin or the seaweed extract by at least two-fold (FIC index= 0.50-0.75) which revealed additive activity against *E. faecalis*. These findings demonstrate the promising antibacterial potential of seaweed extracts and the binary combinations with ciprofloxacin against *E. faecalis*. Future studies will investigate their antibiofilm activity, evaluate their antioxidant potential, and determine their chemical compositions using Gas Chromatography-Mass Spectrometry (GC–MS) analysis.

Keywords: Antibacterial, Ciprofloxacin, *E. faecalis*, *Padina pavonica*, Synergy.

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P67

Investigation of the antiproliferative effect *Xanthoparmelia protomatrae* lichen extract on breast cancer cell lines

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Xanthoparmelia, belonging to the Parmeliaceae family and generally distributed with high diversity in the Southern Hemisphere, is represented by more than 800 species worldwide[1]. *Xanthoparmelia* species are used in traditional medicine for the treatment of impetigo, thrush, gum problems, cancer, heart and urinary tract disorders [2]. This study aimed to determine the antiproliferative activity of a 70% methanol extract of *Xanthoparmelia protomatrae* in breast cancer cells. The cytotoxic activity of the extracts was measured by the MTT method and the results were evaluated as a function of concentration. In the MCF-7 cell line, it was determined that a strong inhibition of 59.36% was created at a concentration of 3.9 µg/mL at the end of 24 hours. In the MDA-MB-231 cell line, the measured inhibition percentages were found to be higher compared to the MCF-7 cell line. Statistically significant inhibition percentages were recorded across the entire concentration range studied (3.9-1000 µg/mL) at the end of 24 hours. Significant inhibition percentages ($p<0.05$) were observed at 48 and 72 hours, at the latest values of 62.5 µg/mL and 31.25 µg/mL, respectively. In conclusion, the promising cytotoxic activity of *X. protomatrae* can form a basis for the development of naturally derived cancer drugs by being evaluated through further pharmacognostic studies.

Keywords: Cytotoxicity, Lichen, *Xanthoparmelia*

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In silico evaluations of pharmacokinetics and toxicity properties of some hydroxycinnamic acids

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Computational *in silico* tools accelerate drug discovery by predicting pharmacological profiles. This study evaluated the ADMET properties, druglikeness, safety, target prediction, and target class distribution of nine hydroxycinnamic acid (HCA) derivatives.
Predictions were executed using pkCSM for ADMET parameters, organ toxicity, and CYP450 interactions, alongside SwissADME for physicochemical properties, druglikeness rules, and BOILED-Egg models. SwissTargetPrediction was utilized for target prediction and target class distribution mapping based on 2D/3D structural similarity.
Low-molecular-weight HCAs (cinnamic, coumaric isomers, caffeic, ferulic acids) demonstrated superior oral bioavailability, high intestinal absorption, and full druglikeness compliance. Cinnamic acid uniquely penetrated the blood-brain barrier. Esterified derivatives (chlorogenic and rosmarinic acids) showed restricted absorption and P-glycoprotein substrate affinity. Toxicity screens confirmed non-mutagenic, non-hepatotoxic profiles without CYP450 interactions. Target prediction and class distribution analyses indicated that HCAs primarily interact with essential enzymes (carbonic anhydrases, aldo-keto reductases, matrix metalloproteinases), lyases, and G-protein coupled receptors.
Hydroxycinnamic acid derivatives exhibit favorable pharmacokinetics, high safety, and distinct target profiles, validating their therapeutic potential.

Keywords: Hydroxycinnamic Acid, ADMET, Target Prediction, In Silico.

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P69

Chemical characterization of *Cymbopogon citratus* essential oil and development of essential oil-loaded solid lipid nanoparticles

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Cymbopogon citratus (DC.) Stapf, a member of the Poaceae family, is an aromatic plant commonly known as lemongrass. Lemongrass grows naturally in India, Africa, South America, and Indonesia. It is widely used in the pharmaceutical industry for the production of cosmetics and perfumes, and in the food industry as a flavoring agent in various dishes [1,2]. The leaves, aerial parts, and roots of *C. citratus* are utilized in cosmetic and perfumery products. In traditional Chinese medicine, it is known for its antipyretic, analgesic, antispasmodic, diuretic, and sedative properties [3,4]. Thirteen primary components were analyzed using gas chromatography–mass spectrometry. The major components were geraniol acetate (50.81%), citral (16.97%), β-citral (12.95%), and geranial (9.45%). *Cymbopogon citratus* essential oil-loaded PLGA nanoparticles were prepared using the nanoprecipitation (solvent displacement) method [5]. Blank nanoparticles exhibited a mean particle size of 150.5 ± 1.2 nm, a polydispersity index (PDI) of 0.11, and a zeta potential of −17.9 ± 0.68 mV. Encapsulation of *Cymbopogon citratus* essential oil resulted in an increase in particle size to 165.6 ± 0.45 nm, while the PDI remained unchanged at 0.11. The zeta potential of the essential oil-loaded nanoparticles was determined to be −17.7 ± 0.06 mV.

Keywords:

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NOT PRESENTED

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Investigation of the biological activities of *Prangos ferulacea* at different phenological stages

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Prangos ferulacea (L.) Lindl. is a perennial aromatic plant belonging to the Apiaceae family and is naturally distributed throughout the Eastern Mediterranean and Western Asia. In traditional medicine, it has been used as a carminative, tonic, and emollient for the treatment of gastrointestinal disorders, as well as for its anti-inflammatory, antibacterial, and antifungal properties. Phytochemical studies have demonstrated that *P. ferulacea* possesses a rich phytochemical profile, particularly in coumarins, alkaloids, terpenoids, and flavonoids, which are associated with various biological activities, including antioxidant, antimicrobial, analgesic, antidiabetic, and antispasmodic effects [1]. However, comparative studies investigating the biological activities of *P. ferulacea* at different phenological stages remain limited. Therefore, the present study aimed to comparatively evaluate the in vitro antioxidant activities and cytotoxic effects of 70% ethanol extracts prepared from *P. ferulacea* collected at the pre-flowering, flowering, and post-flowering stages. Total phenolic and total flavonoid contents of the extracts were determined using spectrophotometric methods, while their antioxidant activities were evaluated by DPPH and ABTS radical scavenging assays. In addition, the cytotoxic effects of the extracts were assessed on MCF-7 and MDA-MB-231 cell lines using the MTT assay at concentrations ranging from 3.96 to 1000 µg/mL. The post-flowering extract exhibited the highest antioxidant activity, showing 76.08% DPPH radical scavenging activity at 50 µg/mL and an ABTS radical scavenging capacity of 1.12 ± 0.11 mmol Trolox equivalents/L at 10 µg/mL. The highest cytotoxic activity against the MCF-7 cell line was observed for the post-flowering extract, whereas the pre-flowering extract demonstrated the greatest cytotoxic effect against the MDA-MB-231 cell line. These findings indicate that the biological activities of P. ferulacea vary according to its phenological stage, with extracts obtained during the pre-flowering and post-flowering stages exhibiting superior antioxidant and cytotoxic activities. The results suggest that *P. ferulacea* has promising therapeutic potential and warrants further investigation.

Keywords: *Prangos ferulacea*, Antioxidant, Cytotoxicity, Apiaceae

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Chemical compositions and biological activities of *Dittrichia* species growing in Northern Cyprus

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The genus *Dittrichia* Greuter (*Inula* L.), belonging to the family Asteraceae (Compositae), is locally known by common names such as "*sümenit*," "*acı ot*," and "*yapışkan andız otu*" [1, 2, 3]. This genus is predominantly distributed across Africa, Asia, and Europe, particularly within the Mediterranean basin [4]. In the present study, the *in-vitro* anti-inflammatory activities of the taxa growing in Northern Cyprus namely *Dittrichia graveolens* (L.) Greuter subsp. *graveolens* and *D. viscosa* subsp. *angustifolia* (Bég.) Greuter were evaluated, and phytochemical analyses were conducted to identify the compounds responsible for this activity. Volatile and non-volatile constituents from the aerial parts were obtained via hydrodistillation and sequential extraction (*n*-hexane, ethyl acetate, methanol), respectively, followed by chemical analysis. Based on crude extract activity assays, active fractions were isolated from the most potent species using Bioassay-Guided Fractionation (BGF) on an LPS induced in-vitro RAW 264.7 cell line inflammation model. Anti-inflammatory screening and isolation studies on the highly effective methanol ethyl acetate fraction of *D. graveolens* subsp. *graveolens* yielded 10 pure compounds. The chemical compositions of the essential oils were determined by GC and GC-MS methods. Furthermore, acute and chronic toxicity levels of both the essential oils and the methanol extracts were evaluated *in-vivo* using *Caenorhabditis elegans* as an alternative animal model.

Keywords: Asteraceae, Anti-inflammatory activity, *Dittrichia*, Phytochemical analysis

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Evaluation of the cannabinoid receptor binding affinity of *Corchorus olitorius* leaf extracts and subfractions

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Corchorus olitorius L. (Malvaceae), or molokhia, is traditionally used in the Eastern Mediterranean and Cyprus to manage inflammatory pain. However, its molecular interactions with the endocannabinoid system (ECS), specifically cannabinoid receptors type 1 (CB1) and type 2 (CB2), remain unexplored. This study evaluates the *in vitro* binding affinity of *C. olitorius* leaf extracts and chromatographic subfractions toward human CB1 and CB2 receptors.

Dried leaves (100 g) from Famagusta, Northern Cyprus, were extracted with 70% methanol. The aqueous residue was partitioned to yield dichloromethane (DCM) and n-butanol extracts (2.04% yield). The *n*-butanol extract was fractionated via Sephadex LH-20 column chromatography, yielding 11 consolidated subfractions (Fractions 12–54) tracked by thin-layer chromatography (TLC). The crude DCM extract and n-butanol subfractions were evaluated using a radioligand displacement assay on transfected CHO cell membranes overexpressing human CB1 or CB2 receptors, utilizing [^{3}H]SR141716A (CB1) and [^{3}H]WIN55,212-2 (CB2).

The crude DCM extract exhibited strong binding potency for both receptors, with an EC_{50} of 4.75 x 10^{-6} mol/L (K_i = 3.21 x 10^{-6} mol/L) at CB1, and an EC_{50} of 9.68 x 10^{-6} mol/L (K_i = 5.44 x 10^{-6} mol/L) at CB2. Among the n-butanol elution, advanced less-polar fractions showed superior concentration-dependent displacement. Fraction 49–54 displayed a prominent nanomolar-range affinity with an EC_{50} of 3.60 x 10^{-6} mol/L (K_i = 2.43 x 10^{-6} mol/L) for CB1. For CB2, Fractions 45–48 and 49–54 achieved substantial displacement, highlighting a concentration of active compounds in these specific segments. This study demonstrates for the first time that lipophilic and moderately polar phytochemical segments of *C. olitorius* directly interact with human CB1 and CB2 receptors. Phytochemical compositional evaluations are ongoing with LC/MS/MS methodology. These findings provide a molecular basis for the traditional use of this plant as an analgesic and anti-inflammatory agent.

Keywords: *Corchorus olitorius*, Cannabinoid Receptors, Radioligand Binding, Subfractionation, Analgesic.

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Cytotoxic potential of crude extract and fractions of endemic *Centaurea ertugruliana* on MCF-7 breast cancer cells

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The genus *Centaurea* L., belonging to the tribe *Cardueae* within the Asteraceae family, encompasses 777 species worldwide, especially in the Americas, Europe, North Africa, and Asia. The presence of 206 taxa in the genus *Centaurea* in Türkiye, with 67% being endemic, signifies that Türkiye is an important center of species diversity for *Centaurea* [1]. *Centaurea* species have considerable phytochemical diversity, particularly in sesquiterpene lactones, flavonoids, phenolic acids, lignans, and essential oils, which support their antioxidant, antibacterial, anti-inflammatory, cytotoxic, anticholinesterase, and hepatoprotective activities [2]. In the current study, the methanol extract and its petroleum ether, $CHCl_3$, EtOAc, n-BuOH, and water fractions of endemic *C. ertugruliana* were investigated for their cytotoxic activity against MCF-7 cells by the MTT method. For the positive control, the cells were treated with the chemotherapeutic drug cisplatin, which has been widely used in a range of cancers. According to the results, the $CHCl_3$ fraction of the methanol extract is the most active sample, and it has moderate cytotoxic activity with 31.00±1.24 µg/mL IC_{50} values on MCF-7 cells. All the tested extracts and fractions, except water fraction, showed cytotoxic activity in a dose-dependent manner. It is the first cytotoxic activity study of *C. ertugruliana* against MCF-7. Cytotoxicity tests on healthy cells and studies regarding the isolation and structural elucidation of the compounds responsible for the cytotoxic effect are ongoing.

Keywords: *Centaurea*, Cytotoxicity, MCF-7, Breast cancer, MTT

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A comparative study on the biological activity potential of the aerial and root parts of *Huynhia pulchra*

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The genus *Arnebia* Forssk. (Boraginaceae) is characterized by 36 species, primarily distributed in Central Asia, North Africa, and Europe. "*Arnebia pulchra* (Willd. ex Roem. & Schult.) Edm." has recently been reclassified under the taxonomic name *Huynhia pulchra* (Willd. ex Roem. & Schult.) Greuter & Burdet. Commonly known as "güzel eğnik," the plant grows naturally in the Eastern Black Sea Region and the Erzurum-Kars Region [1]. Studies have demonstrated that various *Arnebia* species exhibit a wide range of pharmacological activities, including antimicrobial, antioxidant, anti-inflammatory, antidiabetic, immunomodulatory, cytotoxic, and wound-healing effects [2, 3]. However, no research has been found in the literature evaluating the biological activity of *H. pulchra*. This study aimed to evaluate the antioxidant and cytotoxic effects of *H. pulchra* for the first time. The aerial parts and roots of *H. pulchra* were macerated with 70% ethanol at room temperature for 8 h. The crude ethanol extracts were then subjected to liquid-liquid fractionation in a separating funnel using *n*-hexane and *n*-butanol, respectively. The resulting *n*-hexane, *n*-butanol, and residual water sub-extracts were concentrated under reduced pressure in a rotary evaporator. The anticancer activity of the extracts and sub-extracts against HT-29 and HCT-116 colon cancer cells was assessed using the 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide assay. The 2,2-diphenyl-1-picrylhydrazyl (DPPH) and 2,2'-azino-bis(3-ethylbenzothiazoline-6-sulfonic acid) (ABTS) radical scavenging activities of the samples were also evaluated *in vitro*. The *n*-butanol root sub-extract strongly scavenged the DPPH radical with an IC_{50} value of 146.0 µg/mL. The highest ABTS radical scavenging activity was observed in the ethanol extract of the root, with an IC_{50} value of 154.8 µg/mL. The root and aerial water sub-extracts inhibited HT-29 colon cancer cells with IC_{50} values of 3.86 ± 0.01 and 4.15 ± 0.45 µg/mL, respectively. In HCT-116 cells, the strongest cytotoxic activity was found in the aerial water sub-extract, with a value of 3.81 ± 0.18 µg/mL. In conclusion, *H. pulchra* extracts have demonstrated significant antioxidant and selective cytotoxic activity. Notably, the strong effect of the water sub-extracts on colon cancer cells indicates that these extracts could serve as promising sources for isolating bioactive compounds with potential anticancer properties.

Keywords: *Huynhia pulchra*, Boraginaceae, Antioxidant activity, Cytotoxic activity, Colon cancer

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Evaluation of the antioxidant and cytotoxic activities of *Prangos platychlaena*

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While the Apiaceae family is represented by 511 taxa in Türkiye, the genus *Prangos* is also included in this family. The genus *Prangos* comprises 30 species distributed worldwide. *Prangos* species have been used for centuries not only for their traditional properties as emollients, tonics, carminatives, antispasmodics, and hemorrhoid preventatives, but also for their ability to stop external bleeding and promote wound healing. *Prangos platychlaena* Boiss. is a perennial herb endemic to Türkiye and known locally by the names çağşır, çakşır, korkor or kirkor and traditionally used externally in Eastern Türkiye to stop skin bleeding or heal scars [1]. In this context, the aim of this study was to evaluate the antioxidant activities of 70% ethanol extracts prepared from pre-flowering, flowering, and post-flowering samples of the *Prangos platychlaena* plant, which grows in our country, and to investigate their cytotoxic effects on a human breast cancer cell line. The antioxidant activity of the extracts was evaluated using the DPPH and ABTS radical scavenging assays. The post-flowering extract was identified as the most active extract, exhibiting 76.62% DPPH radical scavenging activity at 200 µg/mL and 0.89 mmol/L Trolox ABTS radical scavenging activity at 10 µg/mL. The cytotoxic activity of the extracts on the MCF-7 (human breast cancer) and MDA-MB-231 (human breast cancer) cell lines was determined using the MTT assay. The post-flowering extract was found to be the most active against the MCF-7 cell line, while the pre-flowering extract was the most active against the MDA-MB-231 cell line. These findings indicate that both pre- and post-flowering extracts exhibit antioxidant activity and also demonstrate concentration dependent cytotoxic effects against breast cancer cell lines. The results suggest that the *Prangos platychlaena* plant may have therapeutic application potential, provided it is supported by further studies.

Keywords: Antioxidant, Apiaceae, *Prangos*, Cytotoxicity

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Evaluation of the correlation between traditional antidiabetic plant use in Antalya and scientific literature

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Diabetes mellitus is a chronic metabolic disorder for which traditional plant-based remedies are widely used as complementary approaches in many local communities [1]. Antalya, located in the Mediterranean region of Türkiye, and this study aimed to compile and evaluate ethnobotanical records of plants traditionally used for diabetes and blood glucose regulation in Antalya province.

Ethnobotanical master's and doctoral theses registered in the Council of Higher Education National Thesis Center (YÖK Thesis Center) and conducted in the cities of the Mediterranean region of Türkiye were reviewed. Plant taxa reported for prostate treatment were compiled and classified according to family, local name, used plant part, uses, preparation method, and references. In addition, each taxon was checked in the scientific literature to determine whether previous studies related to prostate disorders were available.

A comprehensive table was prepared including the plants traditionally used as antidiabetic remedies in Antalya. 46 taxa were listed for uses in traditional medicine and the most cited family was found Rosaceae with 10 taxa. The recorded uses mainly involved internal administration, mostly as infusions or decoctions prepared from primarily fruits of the plants. Comparison with the available literature indicated that 42 taxa were supported by experimental or clinical studies reporting antidiabetic activity, effects on glucose metabolism, enzyme inhibitory potential, or antioxidant properties, whereas several plants lacked direct scientific evidence regarding their traditional use for diabetes.

The findings indicate that Antalya's traditional medicinal plant knowledge may provide valuable clues for identifying candidate taxa for antidiabetic research. The presence of unsupported traditional records highlights the need for further pharmacological investigations.

Keywords: Diabetes mellitus, Ethnobotany, Antidiabetic activity

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In vitro evaluation of the antioxidant and *α*-glucosidase enzyme inhibitor potential of *Loranthus europaeus*

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Diabetes mellitus is a metabolic disorder characterised by high blood sugar levels, resulting from the pancreas's inability to produce enough insulin or the body's cells' inability to respond adequately and effectively to the insulin produced. Uncontrolled hyperglycemia in diabetic patients leads to the development of various complications. While current medications are useful in controlling early-onset complications of diabetes, they are insufficient in preventing disease progression, and due to developing side effects, there is still a need for the development of new antihyperglycemic agents. Various studies have reported that some species belonging to the genus *Loranthus* (Loranthaceae) have potential antidiabetic effects [1-2]. This study evaluated the antidiabetic potential of extracts prepared from the semi-parasitic plant species *Loranthus europaeus* Jacq. using *in vitro* methods, along with their antioxidant activity, and performed phytochemical content analyses of these extracts using HPLC. Experimental results revealed that the ethyl acetate sub-extract obtained from the 80% methanolic extract using the liquid-liquid extraction method showed the highest radical scavenging activity (IC_{50}: 2.74 ± 0.34 µg/mL) against ABTS radical, while the hexane sub-extract showed the highest inhibitory effect (IC_{50}: 81.05 ± 2.22 µg/mL) on α-glucosidase. Parallel to its antioxidant activity, the ethyl acetate sub-extract was also found to have higher total phenolic (425.03 ± 3.32 mg $_{GAE}/g_{extract}$) and total flavonoid content (210.31 ± 3.27 mg $_{CE}/g_{extract}$) compared to the other extracts. HPLC analysis showed that the ethyl acetate sub-extract contained gallic acid, protocatechuic acid, chlorogenic acid, caffeic acid, 4-hydroxycoumaric acid, ferulic acid, benzoic acid, rutin, rosmarinic acid, cinnamic acid, and luteolin, with ferulic acid being the compound with the highest concentration. The data obtained are expected to shed light on studies focusing on the regulation of postprandial hyperglycemia and the development of new agents in the multifaceted treatment of diabetes. Further studies on the plant's antidiabetic efficacy are ongoing.

Keywords: *Loranthus europaeus*, Antioxidant, *α*-Glucosidase

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Investigation of the antioxidant and cytotoxic activity potential of *Prangos uloptera* according to its phenological growth stages

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The genus *Prangos*, belonging to the Apiaceae, is an Iran-Turan element and represented with 19 taxa in Türkiye and 11 taxa are endemic [1]. *Prangos* species are commonly used as tonic and for managing wounds, hemorrhoids, flatulence, and leukoplakia in traditional medicine [2]. This study aimed to determine the biological activities 70% ethanol extract of *Prangos uloptera*, collected at different phenological stages (pre-flowering, flowering period, post-flowering). The antioxidant activity of extracts was measured using DPPH and ABTS radical-scavenging assay and results showed high radical scavenging activity in a dose-dependent manner. The post-flowering extract was found to be the most potent extract, exhibiting 79.66% DPPH radical scavenging activity at 200 µg/mL, and an ABTS radical scavenging activity of 0.86 ± 0.09 mmol Trolox/L at 10 µg/mL. Cytotoxicity evaluations of the extracts were performed on MCF-7 and MDA-MB-231cell lines using the MTT method. All extracts exhibited dose-dependent inhibition of cell viability in the dose range of 3.96-1000 µg/mL. The extract pre-flowering exhibited the strongest cytotoxic effect on the MCF-7 cell line. The chemical composition of the extracts was determined total phenol and flavonoid content analysis. The post-flowering extract was found to have the highest total phenolic content (167.48 ± 3.91 mg GAE/g), the flowering period extract exhibited the highest total flavonoid content (49.12 ± 2.18 mg RE/g extract). In conclusion, *Prangos uloptera* is a promising natural source for further medical studies.

Keywords: Antioxidant, Cytotoxicity, *Prangos*.

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Ethnobotanical potential and sustainable utilization of *Phragmites australis*: A case study on eco-friendly building materials in Akburun Village (Beyşehir, Konya)

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Ethnobotanical investigations serve as a fundamental bridge for documenting traditional botanical knowledge, preserving invaluable biocultural heritage for future generations, and providing critical leads for modern drug discovery [1]. Beyond medicinal applications, traditional ecological knowledge increasingly offers innovative, sustainable solutions to contemporary environmental and economic challenges [2]. Within this framework, based on preliminary field data collected between April 2024 and May 2025 in Akburun Village (Beyşehir, Konya), this study evaluates the ethnobotanical utilization of wetland vegetation, specifically highlighting the structural potential of common reed (*Phragmites australis* (Cav.) Trin. ex Steud.) as a sustainable building material and examining its contribution to the local bio-economy through entrepreneurial initiatives. To achieve this, ethnobotanical field data were gathered through semi-structured interviews with local residents and a key informant entrepreneur, accompanied by the systematic documentation of traditional and contemporary processing techniques of *P. Australis*. The collected specimens were analyzed and taxonomically identifes according to the collections of Herbarium of Istanbul University (ISTE). The findings indicate that local reed biomass historically restricted to basic domestic utility exhibits notable thermal insulation and structural characteristics suitable for modern, eco-friendly construction. Ultimately, through an individual entrepreneurial effort, this traditional resource has been successfully evaluated into a commercialized eco-material, presenting a micro-scale model of a circular bio-economy that integrates local knowledge preservation with sustainable rural development in the Beyşehir basin.

Keywords: Ethnobotany, Eco-friendly, Sustainable, *Phragmites australis*

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P80

Ethnobotanical uses of medicinal plants for prostate disorders in the Mediterranean region of Türkiye: Compatibility with scientific literature

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The use of medicinal plants for the treatment of prostate-related disorders remains an important area of research [1]. Therefore, this study aimed to evaluate the agreement between the traditional use of medicinal plants for prostate-related disorders in the Mediterranean region of Türkiye and the evidence available in scientific literature.

Ethnobotanical master's and doctoral theses registered in the Council of Higher Education National Thesis Center (YÖK Thesis Center) and conducted in the cities of the Mediterranean region of Türkiye were reviewed. Plant taxa reported for prostate treatment were compiled and classified according to family, local name, used plant part, uses, preparation method, and references. In addition, each taxon was checked in the scientific literature to determine whether previous studies related to prostate disorders were available.

A comprehensive table was prepared including the plants traditionally used for prostate complaints in the Mediterranean region. 22 taxa were listed for use in traditional medicine. Hatay was identified to be the most recorded city. The most frequently recorded families were Asparagaceae, Rosaceae, Santalaceae, and Lamiaceae. The recorded uses mainly involved internal administration, mostly as infusions or decoctions consumed as tea. Literature comparison showed that 13 taxa were supported by studies related to prostate disorders, while other plants listed had no direct prostate-related scientific evidence.

The findings indicate that ethnobotanical records may serve as an important preliminary source for identifying candidate plants for prostate-related research. However, the lack of direct experimental evidence for some taxa highlights the need for further pharmacological investigations. This study contributes to the documentation and scientific evaluation of traditional prostate-related plant use in the Mediterranean region of Türkiye.

Keywords: Prostate disorders, Ethnobotany, Pharmacological activity

References:

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P81

An Ethnobotanical survey of Mustafakemalpaşa (Bursa), Türkiye

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Traditional ethnobotanical knowledge provides valuable insights into the relationships between local communities and plants and contributes to the documentation and preservation of biocultural diversity [1]. This research was conducted to identify the plants traditionally used in the Mustafakemalpaşa district of Bursa. Between May 2021 and June 2023, a total of 9 field studies were carried out, amounting to 42 days of fieldwork. During this period, 71 villages in the district were visited, and 197 different plant specimens were collected. Through interviews with 258 people, detailed forms were used to record how these plants were used in the past and present. Information was compiled about the local names of the plants, their uses, which parts were used, preparation methods, application techniques, dosages, and durations of use. The collected plants are preserved at the Herbarium of Istanbul University Faculty of Pharmacy (ISTE). As a result of the study, a total of 132 taxa (115 wild and 17 cultivated) used by the local people were identified. Among their uses, 94 were for medicinal purposes, 82 for food, 12 for veterinary medicine, 10 as animal feed, 5 for beekeeping and sericulture, 4 as dyes, and 20 for other miscellaneous uses. Additionally, the medical usage information obtained was compared with ethnobotanical studies conducted in Türkiye, and it was determined that the medical uses of 15 taxa in this study differ from those reported in the literature. This research is the first comprehensive ethnobotanical study in the region and ensures that traditional knowledge is recorded before it is forgotten. Additionally, new medical uses recorded in the region are also providing a source for future bioactivity studies with these plants.

Keywords: Traditional knowledge, Medicinal plants, Food plants, Mustafakemalpaşa, Bursa

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[1] Berkes, F., Colding, J., & Folke, C. *Ecological Applications*, 2000, 10*(*5), 1251–1262.

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An Ethnobotanical study of medicinal plants in Kürtün (Gümüşhane)

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This research provides valuable insights into medicinal plants used in traditional folk medicine and their ethnopharmacological applications within the Kürtün district of Gümüşhane province, located in the Eastern Black Sea region of Türkiye. The primary objective of the study was to identify and document plant species utilized by local inhabitants for therapeutic purposes and to record traditional knowledge related to herbal remedies. The study is based on plant specimens collected during field excursions conducted in the summer of 2025. The families most frequently represented were Asteraceae (16.7%), followed by Lamiaceae (10.6%), Apiaceae (6.1%), Rosaceae (6.1%), and Boraginaceae (4.5%). Furthermore, the Cultural Importance Index (CI) and use report (UR) were calculated for each recorded taxa. According to the CI values, the most culturally significant plants were *Hypericum perforatum* L., *Urtica dioica* L., *Thymus longicaulis* C. Presl *subsp. longicaulis var. subisophyllus* (Borbas), *Tanacetum parthenium* (L.) Schultz. BIP., and *Plantago major* L. subsp. *major*. Analysis of preparation techniques indicated that infusion was the most common method (26.31%), followed by direct use (17.54%), decoction (14.03%), poultice (7.01%), and various other preparation methods (35.11%). Ethnopharmacological findings revealed that these medicinal plants are mainly employed in the treatment of respiratory, digestive, skin, and musculoskeletal disorders. Overall, the results demonstrate that traditional medicinal practices remain active within rural communities of Northeastern Anatolia and underline the importance of preserving this valuable local knowledge, which continues to contribute significantly to primary healthcare in the region.

Keywords: Ethnobotanical study, Ethnopharmacology, Medicinal plants, Traditional knowledge, Türkiye

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P83

Centaurea in the Turkish ethnobotanical literature: A comprehensive analysis of their traditional uses

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Centaurea L. (Asteraceae) is an important plant genus characterized by high species diversity in Türkiye. This study aimed to compile ethnobotanical data on *Centaurea* species used in traditional practices in Türkiye and to identify the major patterns of their traditional uses. Master's and doctoral theses published between 1988 and 2026 and included in the National Thesis Center database of the Council of Higher Education were searched using the keyword "ethnobotany." A total of 80 relevant theses containing records of the genus *Centaurea* were examined. From 75 theses that included original fieldwork data and documented uses of *Centaurea* species, 147 ethnobotanical records were compiled. Data derived from secondary literature, records lacking information on use, and taxonomically uncertain records were excluded from the analysis. The records were examined with respect to taxon identity, the region in which the use was documented, the local name, the plant part used, and the purpose of use. Among the records examined, *Centaurea iberica* (n=31) was the most frequently reported taxon, followed by *C. solstitialis* (n=30), *C. virgata* (n=17), and *C. depressa* (n=14). The most frequently reported therapeutic uses were for gastrointestinal disorders (n=26), wounds and dermatological conditions (n=21), renal and urinary tract disorders (n=11), diabetes (n=9), respiratory ailments (n=8), fever (n=5), malaria (n=5), and hemorrhoids (n=4). Non-therapeutic uses included use as food and animal feed, broom-making, decorative purposes, natural dyeing, apiculture, and sericulture. The aerial parts, whole plant, leaves, and flowers were the most frequently used plant materials. The findings demonstrate that *Centaurea* species occupy an important place in the traditional botanical knowledge of Türkiye, both for therapeutic purposes and in everyday practices.

Keywords: *Centaurea*, Asteraceae, Ethnobotany

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Ethnobotanical research in Demircili and Yeniköy villages (Izmir-Türkiye)

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This preliminary ethnobotanical study was carried out between 2025 and 2026 in Demircili and Yeniköy villages of the Ödemiş district, situated in the southeastern part of İzmir Province in western Türkiye. The findings of this study provide information on the main traditional medicinal plants, wild food plants, and other plant uses among the local inhabitants of the study area. The primary objective of this study was to collect, identify, and provide information about plants traditionally used by the local population. This inquiry focused on the plant specimens obtained during field work. Information on the local names of plants, names of the part(s) of the plants used, the methods of preparation and modes of consumption was obtained through face-to-face interviews with the local inhabitants of the region. Collected plants were identified. Voucher specimens were deposited at the Herbarium of the Faculty of Pharmacy at Marmara University (MARE). A total of 45 taxa of plants used in folk medicine, belonging to 26 families, were identified in this study. Of these, 30 taxa were wild and 15 were cultivated. The most common families were Asteraceae, Rosaceae, Lamiaceae, Malvaceae and Moraceae. Based on the results of this study, 45 taxa with ethnobotanical uses were recorded. The plants were used as folk medicine (40 taxa), as food (17 taxa), and for other purposes (6 taxa). This study determined that plants are still traditionally used in the region.

Keywords: Ethnobotany, Izmir, Odemis, Pharmaceutical Botany, Türkiye.

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Ethnobotanical uses of *Thymus* species growing in Türkiye

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Thymus species are among the most widely used members of Lamiaceae in Türkiye from an ethnobotanical point of view; they are used in the treatment of various diseases, especially respiratory and digestive system disorders. [1] In Türkiye, the genus Thymus is represented by approximately 42 species. [2] This study comprehensively evaluated the ethnobotanical characteristics of taxa belonging to the genus *Thymus* that naturally occur in Türkiye and are traditionally used by local communities. A total of 278 ethnobotanical studies were examined, of which 162 provided data regarding the use of *Thymus* taxa. Based on the obtained findings, a total of 30 taxa used among the local population were identified. Among these taxa, 27 were reported for medicinal purposes, 25 for food use, 5 as animal feed, 5 for cosmetic purposes, 3 for apicultural use, 2 for belief-related practices, 2 as insecticides, and 1 for commercial purposes. The most frequently reported taxa were *Thymus sipyleus* Boiss. (31 references), *Thymus longicaulis* subsp. *chaubardii* (Rchb.f.) Jalas (14 references), and *Thymus kotschyanus* subsp. *kotschyanus* Boiss. & Hohen. (14 references). The most commonly reported medicinal uses were associated with digestive system disorders (stomachache, diarrhea, gastritis), respiratory diseases (cough, asthma, bronchitis), and conditions related to pain and inflammation (rheumatism and muscle pain). In medicinal applications, the aerial parts were the most frequently utilized plant parts, and the taxa were predominantly consumed in the form of infusions. In terms of food use, these taxa were mainly consumed as spices and herbal teas, with aerial parts again being the most commonly used components. This study systematically documents the traditional uses of *Thymus* taxa, contributes to the integration of ethnobotanical data with existing pharmacological and phytochemical studies, and provides a foundation for future interdisciplinary research.

Keywords: *Thymus*, Ethnobotany, Traditional medicine, Edible plants, Türkiye

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From traditional knowledge to scientific evidence: Plants used for rheumatism in Osmaniye, Hatay and Kahramanmaraş

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Rheumatic complaints are among the common health problems for which traditional plant-based remedies are frequently used in local communities [1]. The present study was based on ethnobotanical data concerning medicinal plants traditionally used for rheumatism in Kahramanmaraş, Hatay, and Osmaniye provinces of the Eastern Mediterranean region of Türkiye.

Ethnobotanical master's and doctoral theses registered in the Council of Higher Education National Thesis Center (YÖK Thesis Center) and conducted in the cities of the Mediterranean region of Türkiye were reviewed. Plant taxa reported for prostate treatment were compiled and classified according to family, local name, used plant part, uses, preparation method, and references. In addition, each taxon was checked in the scientific literature to determine whether previous studies related to prostate disorders were available.

Medicinal plants traditionally used for rheumatic complaints in Kahramanmaraş, Hatay, and Osmaniye were organized in a comprehensive table. In total, 26 taxa were listed based on their traditional medicinal use, and Hatay was found the most recorded city in the study. The records included both internal and external uses, commonly in the form of infusions, decoctions, poultices, oils, or direct topical applications prepared from various plant parts. Literature comparison showed that 24 taxa were supported by anti-inflammatory, analgesic, or antioxidant studies, whereas others lacked direct scientific evidence related to rheumatic conditions.

The results demonstrate that antirheumatic plant use in these Mediterranean provinces reflects a valuable local therapeutic tradition. The presence of both literature-supported and insufficiently investigated taxa suggests that these records may guide future studies focusing on bioactivity, active compounds, and pharmacology.

Keywords: Rheumatism, Ethnobotany, Analgesic, Anti-inflammatory

References:

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Rediscovery of *Linum corymbiferum* in Europe

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Linum corymbiferum, a species treated as historic casual in France, was rediscovered in the department Gard, on its previously documented location and several close places. This species, endemic to Algeria and Tunisia, was discovered in 1875 in Rodilhan (department Gard, France) by A. Barrandon, J. Duval-Jouve and Courcière. It was then recorded four times at the same location in the following years by different botanists who collected samples. Other herbarium specimens dated 1872, 1913 and 1927 were respectively collected in Hyères (department Var, France and Béziers (department Hérault, France). Subsequently, the species had not been recorded in Europe until 2025.

Keywords: floristics, alien flora, France.


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